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(54) Title: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND METHODS OF USE THEREOF (57) Abstract <p>Nucleic acid sequences encoding ϵ-cyclase, isopentenyl pyrophosphate isomerase and β-carotene hydroxylase as well as vectors containing the same and hosts transformed with the vectors. Methods for controlling the ratio of various carotenoids in a host and for the production of novel carotenoid pigments. The present invention also provides a method for screening for eukaryotic genes encoding carotenoid biosynthesis, and for modifying the disclosed enzymes.</p>		

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GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

Field of the Invention

5 The present invention describes nucleic acid sequences for eukaryotic genes encoding ϵ lycopene ϵ -cyclase (also known as ϵ -cyclase and ϵ lycopene cyclase), isopentenyl pyrophosphate isomerase (IPP) and β -carotene hydroxylase as well as vectors containing the same and hosts transformed with said vectors. The present invention also provides methods for augmenting the accumulation of carotenoids, changing the composition of the

10 carotenoids, and producing novel and rare carotenoids. The present invention provides methods for controlling the ratio or relative amounts of various carotenoids in a host. The invention also relates to modified lycopene ϵ -cyclase, IPP isomerase and β -carotene hydroxylase. Additionally, the present invention provides a method for screening for genes and cDNAs encoding enzymes of carotenoid biosynthesis and metabolism.

Background of the Invention

15 Carotenoid pigments with cyclic endgroups are essential components of the photosynthetic apparatus in oxygenic photosynthetic organisms (e.g., cyanobacteria, algae and plants; Goodwin, 1980). The symmetrical bicyclic yellow carotenoid pigment β -carotene (or, in rare cases, the asymmetrical bicyclic α -carotene) is intimately associated with

20 the photosynthetic reaction centers and plays a vital role in protecting against potentially lethal photooxidative damage (Koyama, 1991). β -carotene and other carotenoids derived from it or from α -carotene also serve as light-harvesting pigments (Siefermann-Harms, 1987), are involved in the thermal dissipation of excess light energy captured by the light-harvesting antenna (Demmig-Adams & Adams, 1992), provide substrate for the biosynthesis

25 of the plant growth regulator abscisic acid (Rock & Zeevaart, 1991; Parry & Horgan, 1991), and are precursors of vitamin A in human and animal diets (Krinsky, 1987). Plants also exploit carotenoids as coloring agents in flowers and fruits to attract pollinators and agents of seed dispersal (Goodwin, 1980). The color provided by carotenoids is also of agronomic value in a number of important crops. Carotenoids are currently harvested from a variety of

30 organisms, including plants, algae, yeasts, cyanobacteria and bacteria, for use as pigments in food and feed.

The probable pathway for formation of cyclic carotenoids in plants, algae and cyanobacteria is illustrated in Figure 1. Two types of cyclic endgroups or rings are commonly found in higher plant carotenoids, these are referred to as the β (*beta*) and ϵ (*epsilon*) rings (Fig. 3). The precursor acyclic endgroup (no ring structure) is referred to as the Ψ (*psi*) endgroup. The β and ϵ endgroups differ only in the position of the double bond in the ring. Carotenoids with two β rings are ubiquitous, and those with one β and one ϵ ring are common, but carotenoids with two ϵ rings are uncommon. β -carotene (Fig. 1) has two β -endgroups and is a symmetrical compound that is the precursor of a number of other important plant carotenoids such as zeaxanthin and violaxanthin (Fig. 2).

Genes encoding enzymes of carotenoid biosynthesis have previously been isolated from a variety of sources including bacteria (Armstrong et al., 1989, Mol. Gen. Genet. 216, 254-268; Misawa et al., 1990, J. Bacteriol., 172, 6704-12), fungi (Schmidhauser et al., 1990, Mol. Cell. Biol. 10, 5064-70), cyanobacteria (Chamovitz et al., 1990, Z. Naturforsch., 45c, 482-86; Cunningham et al., 1994) and higher plants (Bartley et al., Proc. Natl. Acad. Sci USA 88, 6532-36; Martinez-Ferez & Vioque, 1992, Plant Mol. Biol. 18, 981-83). Many of the isolated enzymes show a great diversity in structure, function and inhibitory properties between sources. For example, phytoene desaturases from the cyanobacterium *Synechococcus* and from higher plants and green algae carry out a two-step desaturation to yield ζ -carotene as a reaction product. In plants and cyanobacteria a second enzyme (ζ -carotene desaturase), similar in amino acid sequence to the phytoene desaturase, catalyzes two additional desaturations to yield lycopene. In contrast, a single desaturase enzyme from *Erwinia herbicola* and from other bacteria introduces all four double bonds required to form lycopene. The *Erwinia* and other bacterial desaturases bear little amino acid sequence similarity to the plant and cyanobacterial desaturase enzymes, and are thought to be of unrelated ancestry. Therefore, even with a gene in hand from one source, it may be difficult to identify a gene encoding an enzyme of similar function in another organism. In particular, the sequence similarity between certain of the prokaryotic and eukaryotic genes encoding enzymes of carotenoid biosynthesis is quite low.

Further, the mechanism of gene expression in prokaryotes and eukaryotes appears to differ sufficiently such that one cannot expect that an isolated eukaryotic gene will be properly expressed in a prokaryotic host.

The difficulties in isolating genes encoding enzymes with similar functions is exemplified by recent efforts to isolate the gene encoding the enzyme that catalyzes the formation of β -carotene from the acyclic precursor lycopene. Although a gene encoding an enzyme with this function had been isolated from a bacterium, it had not been isolated from any photosynthetic procaryote or from any eukaryotic organism. The isolation and characterization of the enzyme catalyzing formation of β -carotene in the cyanobacterium *Synechococcus* PCC7942 was described by the present inventors and others (Cunningham et al., 1993 and 1994). The amino acid sequence similarity of the cyanobacterial enzyme to the various bacterial lycopene β -cyclases is so low (*ca.* 18-25% overall; Cunningham et al., 1994) that there is much uncertainty as to whether they share a common ancestry or, instead, represent an example of convergent evolution.

The need remains for the isolation of eukaryotic and prokaryotic genes and cDNAs encoding polypeptides involved in the carotenoid biosynthetic pathway, including those encoding a lycopene ϵ -cyclase, IPP isomerase and β -carotene hydroxylase. There remains a need for methods to enhance the production of carotenoids, to alter the composition of carotenoids, and to reduce or eliminate carotenoid production. There also remains a need in the art for methods for screening for genes and cDNAs encoding enzymes of carotenoid biosynthesis and metabolism.

SUMMARY OF THE INVENTION

Accordingly, a first object of this invention is to provide purified and/or isolated nucleic acids which encode enzymes involved in carotenoid biosynthesis; in particular, lycopene ϵ -cyclase, IPP isomerase and β -carotene hydroxylase.

A second object of this invention is to provide purified and/or isolated nucleic acids which encode enzymes which produce novel or uncommon carotenoids.

A third object of the present invention is to provide vectors containing said genes.

A fourth object of the present invention is to provide hosts transformed with said vectors.

Another object of the present invention is to provide hosts which accumulate novel or uncommon carotenoids or which accumulate greater amounts of specific or total carotenoids.

Another object of the present invention is to provide hosts with inhibited and/or altered carotenoid production.

Another object of this invention is to secure the expression of eukaryotic carotenoid-related genes in a recombinant prokaryotic host.

Yet another object of the present invention is to provide a method for screening for eukaryotic and prokaryotic genes and cDNAs which encode enzymes involved in carotenoid biosynthesis and metabolism.

An additional object of the invention is to provide a method for manipulating carotenoid biosynthesis in photosynthetic organisms by inhibiting the synthesis of certain enzymatic products to cause accumulation of precursor compounds.

Another object of the invention is to provide modified lycopene ϵ -cyclase, IPP isomerase and β -carotene hydroxylase.

These and other objects of the present invention have been realized by the present inventors as described below.

A subject of the present invention is an isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity and having the amino acid sequence of SEQ ID NOS: 2, 4, 14-21 or 23-27.

The invention also includes vectors which comprise any of the nucleic acid sequences listed above, and host cells transformed with such vectors.

Another subject of the present invention is a method of producing or enhancing the production of a carotenoid in a host cell, comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence to produce the protein.

Yet another subject of the present invention is a method of modifying the production of carotenoids in a host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which produces an RNA and/or encodes for a protein which modifies lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity, relative to an untransformed host cell, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence in the host cell to modify the production of the carotenoids in the host cell, relative to the untransformed host cell.

The present invention also includes a method of expressing, in a host cell, a heterologous nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity, the method comprising inserting into the host cell a vector comprising the heterologous nucleic acid sequence, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence.

Also included is a method of expressing, in a host cell, a heterologous nucleic acid sequence which encodes for a protein which modifies lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity in the host cell, relative to an untransformed host cell, the method comprising inserting into the host cell a vector comprising the heterologous nucleic acid sequence, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence.

Another subject of the present invention is a method for screening for genes and cDNAs which encode enzymes involved in carotenoid biosynthesis and metabolism.

BRIEF DESCRIPTION OF THE DRAWINGS

A more complete appreciation of the invention and many of the attendant advantages thereof will be readily obtained as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings, wherein:

Figure 1 is a schematic representation of the putative pathway of β -carotene biosynthesis in cyanobacteria, algae and plants. The enzymes catalyzing various steps are indicated at the left. Target sites of the bleaching herbicides NFZ and MPTA are also indicated at the left. Abbreviations: DMAPP, dimethylallyl pyrophosphate; FPP, farnesyl pyrophosphate; GGPP, geranylgeranyl pyrophosphate; GPP, geranyl pyrophosphate; IPP, isopentenyl pyrophosphate; LCY, lycopene cyclase; MVA, mevalonic acid; MPTA, 2-(4-methylphenoxy)triethylamine hydrochloride; NFZ, norflurazon; PDS, phytoene desaturase; PSY, phytoene synthase; ZDS, ζ -carotene desaturase; PPPP, prephytoene pyrophosphate.

Figure 2 depicts possible routes of synthesis of cyclic carotenoids and common plant and algal xanthophylls (oxycarotenoids) from neurosporene. Demonstrated activities of the β - and ϵ -cyclase enzymes of *A. thaliana* are indicated by bold arrows labelled with β or ϵ respectively. A bar below the arrow leading to ϵ -carotene indicates that the enzymatic

activity was examined but no product was detected. The steps marked by an arrow with a dotted line have not been specifically examined. Conventional numbering of the carbon atoms is given for neurosporene and α -carotene. Inverted triangles (∇) mark positions of the double bonds introduced as a consequence of the desaturation reactions.

Figure 3 depicts the carotene endgroups which are found in plants.

Figure 4 is a DNA sequence and the predicted amino acid sequence of a lycopene ϵ -cyclase cDNA isolated from *A. thaliana* (SEQ ID NOS: 1 and 2). These sequences were deposited under Genbank accession number U50738. This cDNA is incorporated into the plasmid pATeps.

Figure 5 is a DNA sequence encoding the β -carotene hydroxylase isolated from *A. thaliana* (SEQ ID NO: 3). This cDNA is incorporated into the plasmid pATOHB.

Figure 6 is an alignment of the predicted amino acid sequences of *A. thaliana* β -carotene hydroxylase (SEQ ID NO: 4) with those of the bacterial β -carotene hydroxylase enzymes from *Alicyobacterium sp.* (SEQ ID NO: 5) (Genbank D58422), *Erwinia herbicola* Eho10 (SEQ ID NO.: 6) (GenBank M872280), *Erwinia uredovora* (SEQ ID NO.: 7) (GenBank D90087) and *Agrobacterium aurianticum* (SEQ ID NO.: 8) (GenBank D58420). A consensus sequence is also shown. All five genes are identical where a capital letter appears in the consensus. A lowercase letter indicates that three of five, including *A. thaliana*, have the identical residue. TM; transmembrane.

Figure 7 is a DNA sequence of a cDNA encoding an IPP isomerase isolated from *A. thaliana* (SEQ ID NO: 9). This cDNA is incorporated into the plasmid pATDP5.

Figure 8 is a DNA sequence of a second cDNA encoding another IPP isomerase isolated from *A. thaliana* (SEQ ID NO: 10). This cDNA is incorporated into the plasmid pATDP7.

Figure 9 is a DNA sequence of a cDNA encoding an IPP isomerase isolated from *Haematococcus pluvialis* (SEQ ID NO: 11). This cDNA is incorporated into the plasmid pHP04.

Figure 10 is a DNA sequence of a second cDNA encoding another IPP isomerase isolated from *Haematococcus pluvialis* (SEQ ID NO: 12). This cDNA is incorporated into the plasmid pHP05.

Figure 11 is an alignment of the amino acid sequences predicted by IPP isomerase cDNAs isolated from *A. thaliana* (SEQ ID NO.: 16 and 18), *H. pluvialis* (SEQ ID NOS.: 14

and 15), *Clarkia breweri* (SEQ ID NO.: 17) (See, Blanc & Pichersky, Plant Physiol. (1995) 108:855; Genbank accession no. X82627) and *Saccharomyces cerevisiae* (SEQ ID NO.: 19) (Genbank accession no. J05090).

Figure 12 is a DNA sequence of the cDNA encoding an IPP isomerase isolated from *Tagetes erecta* (marigold; SEQ ID NO: 13). This cDNA is incorporated into the plasmid pPMDP1. xxx's denote a region not originally sequenced. Figure 21A shows the complete marigold sequence.

Figure 13 is an alignment of the consensus sequence of four plant β -cyclases (SEQ ID NO.: 20) with the *A. thaliana* lycopene ϵ -cyclase (SEQ ID NO.: 21). A capital letter in the plant β consensus is used where all four β -cyclase genes predict the same amino acid residue in this position. A small letter indicates that an identical residue was found in three of the four. Dashes indicate that the amino acid residue was not conserved and dots in the sequence denote a gap. A consensus for the aligned sequences is given, in capital letters below the alignment, where the β - and ϵ -cyclases have the same amino acid residue. Arrows indicate some of the conserved amino acids that will be used as junction sites for construction of chimeric cyclases with novel enzymatic activities. Several regions of interest including a sequence signature indicative of a dinucleotide-binding motif and two predicted transmembrane (TM) helical regions are indicated below the alignment and are underlined.

Figure 14 shows the nucleotide (SEQ ID NO:22) and amino acid sequences (SEQ ID NO:23) of the *Adonis palaestina* (pheasant's eye) ϵ -cyclase cDNA #5.

Figure 15A shows the nucleotide (SEQ ID NO:24) and amino acid sequences (SEQ ID NO:25) of a potato ϵ -cyclase cDNA. Figure 15B shows the amino acid sequence (SEQ ID NO:26) of a chimeric lettuce/potato lycopene ϵ -cyclase. Amino acids in lower case are from the lettuce cDNA and those in upper case are from the potato cDNA. The product of this chimeric cDNA has ϵ -cyclase activity and converts lycopene to the monocyclic δ -carotene.

Figure 16 shows a comparison between the amino acid sequences of the *Arabidopsis* ϵ -cyclase (SEQ ID NO:27) and the potato ϵ -cyclase (SEQ ID NO:25).

Figure 17A shows the nucleotide sequence of the *Adonis palaestina* Ipi1 (SEQ ID NO:28) and Figure 17B shows the nucleotide sequence of the *Adonis palaestina* Ipi2 (SEQ ID NO: 29).

Figure 18A shows the nucleotide sequence of the *Haematoccus pluvialis* Ipi1 (SEQ ID NO:11) and Figure 18B shows the nucleotide sequence of the *Haematoccus pluvialis* Ipi2 (SEQ ID NO:30).

Figure 19A shows the nucleotide sequence of the *Lactuca sativa* (romaine lettuce) Ipi1 (SEQ ID NO:31) and Figure 19B shows the nucleotide sequence of the *Lactuca sativa* Ipi2 (SEQ ID NO: 32).

Figure 20 shows the nucleotide sequence of the *Chlamydomonas reinhardtii* Ipi1 (SEQ ID NO:33).

Figure 21A shows the nucleotide sequence of the *Tagetes erecta* (marigold) Ipi1 (SEQ ID NO:34) and Figure 21B shows the nucleotide sequence of the *Oryza sativa* (rice) Ipi1 (SEQ ID NO:35).

Figure 22 shows a amino acid sequence alignment of various plant and green algal isopentenyl isomerases (IPI) (SEQ ID NOS:16, 36-45).

Figure 23 shows a comparison between *Adonis palaestina* ϵ -cyclase cDNA #3 and cDNA #5 nucleotide sequences.

Figure 24 shows a comparison between *Adonis palaestina* ϵ -cyclase cDNA #3 and cDNA #5 predicted amino acid sequences.

Figure 25 shows a sequence alignment of various plant β - and ϵ -cyclases. Those sequences outlined in grey denote identical sequences among the ϵ -cyclases. Those sequences outlined in black denote identical sequences among both the β - and ϵ -cyclases.

Figure 26 shows a sequence alignment of the plant ϵ -cyclases from Figure 25. Those sequences outlined in black denote identical sequences among the ϵ -cyclases.

Figure 27 is a dendrogram or "tree" illustrating the degree of amino acid sequence similarity for various lycopene β - and ϵ -cyclases.

Figure 28 shows a comparison between *Arabidopsis* ϵ -cyclase and lettuce ϵ -cyclase predicted amino acid sequences.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention includes an isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity and having the amino acid sequence of SEQ ID NOS: 2, 4, 14-21, 23 or 25-27. Nucleic acids encoding lycopene ϵ -cyclase, β -carotene hydroxylase and IPP

isomerases have been isolated from several genetically distant sources.

The present inventors have isolated nucleic acids encoding the enzyme IPP isomerase, which catalyzes the reversible conversion of isopentenyl pyrophosphate (IPP) to dimethylallyl pyrophosphate (DMAPP). IPP isomerase cDNAs were isolated from the plants
5 *A. thaliana*, *Tagetes erecta* (marigold), *Adonis palaestina* (pheasant's eye), *Lactuca sativa* (romaine lettuce) and from the green algae *H. pluvialis* and *Chlamydomonas reinhardtii*. Alignments of the amino acid sequences predicted by some of these cDNAs are shown in Figures 12 and 22. Plasmids containing some of these cDNAs were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852 on March 4,
10 1996 under ATCC accession numbers 98000 (pHP05 - *H. pluvialis*); 98001 (pMDP1 - marigold); 98002 (pATDP7 - *A. thaliana*) and 98004 (pHP04 - *H. pluvialis*).

The present inventors have also isolated nucleic acids encoding the enzyme β -carotene hydroxylase, which is responsible for hydroxylating the β -endgroup in carotenoids. The nucleic acid of the present invention is shown in SEQ ID NO: 3 and Figure 5. The full
15 length cDNA product hydroxylates both end groups of β -carotene as do products of cDNAs which encode proteins truncated by up to 50 amino acids from the N-terminus. Products of genes which encode proteins truncated between about 60-110 amino acids from the N-terminus preferentially hydroxylate only one ring. A plasmid containing this gene was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD
20 20852 on March 4, 1996 under ATCC accession number 98003 (pATOHB - *A. thaliana*).

The present inventors have also isolated nucleic acids encoding the enzyme lycopene ϵ -cyclase, which is responsible for the formation of ϵ -endgroups in carotenoids. The *A. thaliana* ϵ -cyclase adds an ϵ ring to only one end of the symmetrical lycopene while the related β -cyclase adds a ring at both ends. The *A. thaliana* cDNA of the present invention is
25 shown in Figure 4 and SEQ ID NO: 1. A plasmid containing this gene was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852 on March 4, 1996 under ATCC accession number 98005 (pATeps - *A. thaliana*).

In addition, lycopene ϵ -cyclases have been identified in lettuce and in *Adonis palaestina* (cDNA #5) which encode enzymes that convert lycopene to the bicyclic ϵ -carotene (ϵ,ϵ -carotene). An additional cDNA from *Adonis palaestina* (cDNA #3) encodes a
30 lycopene ϵ -cyclase which converts lycopene into δ -carotene (ϵ,ψ -carotene) and differs from the lycopene ϵ -cyclase which forms bicyclic ϵ -carotene (ϵ,ϵ -carotene) by only 5 amino acids.

One or more of these amino acids may be modified by alteration of the nucleotide sequence in the #5 cDNA to obtain an enzyme which forms the bicyclic ϵ,ϵ -carotene. The sequences of the *Adonis palaestina* and *Arabidopsis thaliana* ϵ -cyclases have about 70% nucleotide identity and about 72% amino acid identity.

5 Initial experiments by the inventors with chimeric genes indicated that the part of the ϵ -cyclase which is responsible for adding 2 ϵ rings to form ϵ,ϵ -carotene is the carboxy terminal portion of the gene. The lettuce ϵ -cyclase adds two ϵ rings to form ϵ,ϵ -carotene. A DNA encoding a partial potato ϵ -cyclase (missing its amino terminal portion), when combined with an amino terminal region from the lettuce ϵ -cyclase gene, produces a
10 monocyclic δ -carotene (ϵ,ψ -carotene). With the discovery of the differences between the *Adonis palaestina* clone #3 and clone #5, the specific amino acids responsible for the addition of an extra ϵ ring have been identified (Figure 24). Specifically, amino acid 55 is Thr in clone #3 and Ser in clone #5, amino acid 210 is Asn in clone #3 and Asp in clone #5, amino acid 231 is Asp in clone #3 and Glu in clone #5, amino acid 352 is Ile in clone #3 and Val in
15 clone #5, and amino acid 524 is Lys in clone #3 and Arg in clone #5. It can be appreciated that these changes are quite conservative, as only one change, at amino acid 210, changes the charge of the protein.

Thus, it is clear that the nucleic acids of the invention encoding the enzymes as presently disclosed may be altered to increase a particularly desirable property of the enzyme,
20 to change a property of the enzyme, or to diminish an undesirable property of the enzyme. Such modifications can be by deletion, substitution, or insertion of one or more amino acids, and can be performed by routine enzymatic manipulation of the nucleic acid encoding the enzyme (such as by restriction enzyme digestion, removal of nucleotides by mung bean nuclease or *Bal31*, insertion of nucleotides by Klenow fragment, and by religation of the
25 ends), by site-directed mutagenesis, or may be accidental, such as by low fidelity PCR or those obtained through mutations in hosts that are producers of the enzymes. These techniques as well as other suitable techniques are well known in the art.

Mutations can be made in the nucleic acids of the invention such that a particular codon is changed to a codon which codes for a different amino acid. Such a mutation is
30 generally made by making the fewest nucleotide changes possible. A substitution mutation of this sort can be made to change an amino acid in the resulting protein in a non-conservative manner (i.e., by changing the codon from an amino acid belonging to a grouping

of amino acids having a particular size or characteristic to an amino acid belonging to another grouping) or in a conservative manner (i.e., by changing the codon from an amino acid belonging to a grouping of amino acids having a particular size or characteristic to an amino acid belonging to the same grouping). Such a conservative change generally leads to less change in the structure and function of the resulting protein. A non-conservative change is more likely to alter the structure, activity or function of the resulting protein. The present invention should be considered to include sequences containing conservative changes which do not significantly alter the activity or binding characteristics of the resulting protein.

The following is one example of various groupings of amino acids:

Amino acids with nonpolar R groups: Alanine, Valine, Leucine, Isoleucine, Proline, Phenylalanine, Tryptophan and Methionine.

Amino acids with uncharged polar R groups: Glycine, Serine, Threonine, Cysteine, Tyrosine, Asparagine and Glutamine.

Amino acids with charged polar R groups (negatively charged at Ph 6.0): Aspartic acid and Glutamic acid.

Basic amino acids (positively charged at pH 6.0): Lysine, Arginine and Histidine.

Another grouping may be those amino acids with phenyl groups: Phenylalanine, Tryptophan and Tyrosine.

Another grouping may be according to molecular weight (i.e., size of R groups).

Particularly preferred substitutions are:

- Lys for Arg and vice versa such that a positive charge may be maintained;
- Glu for Asp and vice versa such that a negative charge may be maintained;
- Ser for Thr such that a free -OH can be maintained; and
- Gln for Asn such that a free NH₂ can be maintained.

Amino acid substitutions may also be introduced to substitute an amino acid with a particularly preferable property. For example, a Cys may be introduced to provide a potential site for disulfide bridges with another Cys. A His may be introduced as a particularly "catalytic" site (i.e., His can act as an acid or base and is the most common amino acid in biochemical catalysis). Pro may be introduced because of its particularly planar structure, which induces β -turns in the protein's structure.

It is clear that certain modifications of SEQ ID NOS: 2, 4, 14-21, 23 or 25-27 can take place without destroying the activity of the enzyme. It is noted especially that truncated

versions of the nucleic acids of the invention are functional. For example, several amino acids (from 1 to about 120) can be deleted from the N-terminus of the lycopene ϵ -cyclases of the invention, and a functional protein can still be produced. This fact is made especially clear from Figure 25, which shows a sequence alignment of several plant ϵ -cyclases. As can be seen from Figure 25, there is an enormous amount of sequence disparity between amino acid sequences 2 to about 50-70 (depending on the particular sequence, since gaps are present). There is less, but also a substantial amount of, sequence dissimilarity between about 50-70 to about 90-120 (depending on the particular sequence). Thereafter, the sequences are fairly conserved, except for small pockets of dissimilarity between about 275-295 to about 285-305 (depending on the particular sequence), and between about 395-415 to about 410-430 (depending on the particular sequence).

The present inventors have found that the amount of the 5' region present in the nucleic acids of the invention can alter the activity of the enzyme. Instead of diminishing activity, truncating the 5' region of the nucleic acids of the invention may result in an enzyme with a different specificity. Thus, the present invention relates to nucleic acids and enzymes encoded thereby which are truncated to within 0-50, preferably 0-25, codons of the 5' initiation codon of their prokaryotic counterparts as determined by alignment maps as discussed below.

For example, when the cDNA encoding *A. thaliana* β -carotene hydroxylase was truncated, the resulting enzyme catalyzed the formation of β -cryptoxanthin as the major product and zeaxanthin as minor product; in contrast to its normal production of zeaxanthin.

The present invention is intended to include those nucleic acid and amino acid sequences in which substitutions, deletions, additions or other modifications have taken place, as compared to SEQ ID NOS: 2, 4, 14-21, 23 or 25-27, without destroying the activity of the enzyme. Preferably, the substitutions, deletions, additions or other modifications take place at the 5' end, or any other of those positions which already show dissimilarity between any of the presently disclosed amino acid sequences (see also Figure 25) or other amino acid sequences which are known in the art and which encode the same enzyme (i.e., lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase).

In each case, nucleic acid and amino acid sequence similarity and identity is measured using sequence analysis software, for example, the Sequence Analysis, Gap, or BestFit software packages of the Genetics Computer Group (University of Wisconsin Biotechnology

Center, 1710 University Avenue, Madison, Wisconsin 53705), MEGAlign (DNASStar, Inc., 1228 S. Park St., Madison, Wisconsin 53715), or MacVector (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, California 95008). Such software uses algorithms to match similar sequences by assigning degrees of identity to various substitutions, deletions, and other modifications, and includes detailed instructions as to useful parameters, etc., such that those of routine skill in the art can easily compare sequence similarities and identities. An example of a useful algorithm in this regard is the algorithm of Needleman and Wunsch, which is used in the Gap program discussed above. This program finds the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. Another useful algorithm is the algorithm of Smith and Waterman, which is used in the BestFit program discussed above. This program creates an optimal alignment of the best segment of similarity between two sequences. Optimal alignments are found by inserting gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman.

Conservative (i.e. similar) substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine and leucine; aspartic acid, glutamic acid, asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. Substitutions may also be made on the basis of conserved hydrophobicity or hydrophilicity (see Kyte and Doolittle, *J. Mol. Biol.* 157: 105-132 (1982)), or on the basis of the ability to assume similar polypeptide secondary structure (see Chou and Fasman, *Adv. Enzymol.* 47: 45-148 (1978)).

If comparison is made between nucleotide sequences, preferably the length of comparison sequences is at least 50 nucleotides, more preferably at least 60 nucleotides, at least 75 nucleotides or at least 100 nucleotides. It is most preferred if comparison is made between the nucleic acid sequences encoding the enzyme coding regions necessary for enzyme activity. If comparison is made between amino acid sequences, preferably the length of comparison is at least 20 amino acids, more preferably at least 30 amino acids, at least 40 amino acids or at least 50 amino acids. It is most preferred if comparison is made between the amino acid sequences in the enzyme coding regions necessary for enzyme activity.

It should be appreciated that also within the scope of the present invention are nucleic acid sequences encoding lycopene ϵ -cyclases, IPP isomerases and β -carotene hydroxylases

which code for enzymes having the same amino acid sequence as SEQ ID NOS: 2, 4, 14-21, 23 or 25-27, but which are degenerate to the nucleic acids specifically disclosed herein.

The amino acid residues described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property of immunoglobulin-binding is retained by the polypeptide.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook et al, "Molecular Cloning: A Laboratory Manual" (1989); "Current Protocols in Molecular Biology" Volumes I-III [Ausubel, R. M., ed. (1994)]; "Cell Biology: A Laboratory Handbook" Volumes I-III [J. E. Celis, ed. (1994)]; "Current Protocols in Immunology" Volumes I-III [Coligan, J. E., ed. (1994)]; "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription And Translation" [B.D. Hames & S.J. Higgins, eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

The present invention also includes vectors. Suitable vectors according to the present invention comprise a nucleic acid of the invention encoding an enzyme involved in carotenoid biosynthesis or metabolism and a suitable promoter for the host, and can be constructed using techniques well known in the art (for example Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989; Ausubel et al., Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York, 1991). Suitable vectors for eukaryotic expression in plants are described in Frey et al., Plant J. (1995) 8(5):693 and Misawa et al, 1994a; incorporated herein by reference. Suitable vectors for prokaryotic expression include pACYC184, pUC119, and pBR322 (available from New England BioLabs, Beverly, MA) and pTrcHis (Invitrogen) and pET28 (Novagen) and derivatives thereof. The vectors of the present invention can additionally contain regulatory elements such as promoters, repressors, selectable markers such as antibiotic resistance genes, etc.

The nucleic acids encoding the carotenoid enzymes as described above, when cloned into a suitable expression vector, can be used to overexpress these enzymes in a plant

expression system or to inhibit the expression of these enzymes. For example, a vector containing the gene encoding lycopene ϵ -cyclase can be used to increase the amount of α -carotene and carotenoids derived from α -carotene (such as lutein and α -cryptoxanthin) in an organism and thereby alter the nutritional value, pharmacology and visual appearance value of the organism.

Therefore, the present invention includes a method of producing or enhancing the production of a carotenoid in a host cell, relative to an untransformed host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence to produce the protein.

The present invention also includes a method of modifying the production of carotenoids in a host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which produces an RNA and/or encodes for a protein which modifies lycopene ϵ -cyclase, IPP isomerase or β -carotene hydroxylase enzyme activity, relative to an untransformed host cell, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence in the host cell to modify the production of the carotenoids in the host cell, relative to the untransformed host cell.

The term "modifying the production" means that the amount of carotenoids produced in the host cell can be enhanced, reduced, or left the same, as compared to the untransformed host cell. In accordance with one embodiment of the present invention, the make-up of the carotenoids (i.e., the specific carotenoids produced) is changed *vis a vis* each other, and this change in make-up may result in either a net gain, net loss, or no net change in the total amount of carotenoids produced in the cell. In accordance with another embodiment of the present invention, the production or the biochemical activity of the carotenoids (or the enzymes which catalyze their formation) is enhanced by the insertion of an enzyme-encoding nucleic acid of the invention. In yet another embodiment of the invention, the production or the biochemical activity of the carotenoids (or the enzymes which catalyze their formation) may be reduced or inhibited by a number of different approaches available to those skilled in the art, including but not limited to such methodologies or approaches as anti-sense (e.g.,

Gray et al (1992) Plant Mol. Biol. 19:69-87), ribozymes (e.g., Wegener et al (1994) Mol. Gen. Genet. 245:465-470), co-suppression (e.g., Fray and Grierson (1993) Plant Mol. Biol. 22:589-602), targeted disruption of the gene (e.g., Schaefer et al. (1997) Plant J. 11:1195-1206), intracellular antibodies (e.g., Rondon and Marasco (1997) Ann. Rev. Microbiol. 51:257-283) or whatever other approaches rely on the knowledge or availability of the nucleic acid or amino acid sequences of the invention and/or portions thereof, to thereby reduce accumulation of carotenoids with ϵ rings and compounds derived from them (for ϵ -cyclase inhibition), or carotenoids with hydroxylated β rings and compounds derived from them (for β -hydroxylase inhibition), or, in the case if IPP isomerase, accumulation of any isoprenoid compound.

Preferably, at least a portion of the nucleic acid sequences used in the methods, vectors and host cells of the invention codes for an enzyme having an amino acid sequence which is at least 85% identical, preferably at least 90%, at least 95% or completely identical to SEQ ID NOS: 2, 4, 14-21, 23 or 25-27. Sequence identity is determined as noted above. Preferably, sequence additions, deletions or other modifications are made as indicated above, so as to not affect the function of the particular enzyme.

In a preferred embodiment, vectors are manufactured which contain a DNA encoding a eukaryotic IPP isomerase upstream of a DNA encoding a second eukaryotic carotenoid enzyme. The inventors have discovered that inclusion of an IPP isomerase gene increases the supply of substrate for the carotenoid pathway; thereby enhancing the production of carotenoid endproducts, as compared to a host cell which is not transformed with such a vector. This is apparent from the much deeper pigmentation in carotenoid-accumulating colonies of *E. coli* which also contain one of the aforementioned IPP isomerase genes when compared to colonies that lack this additional IPP isomerase gene. Similarly, a vector comprising an IPP isomerase gene can be used to enhance production of any secondary metabolite of dimethylallyl pyrophosphate and/or isopentenyl pyrophosphate (such as isoprenoids, steroids, carotenoids, etc.). The term "isoprenoid" is intended to mean any member of the class of naturally occurring compounds whose carbon skeletons are composed, in part or entirely, of isopentyl C_5 units. Preferably, the carbon skeleton is of an essential oil, a fragrance, a rubber, a carotenoid, or a therapeutic compound, such as paclitaxel.

A vector containing the cDNA encoding a lycopene ϵ -cyclase of the invention, preferably the lettuce lycopene ϵ -cyclase or Adonis ϵ -cyclase #5, can be used to increase the

amount of bicyclic ϵ -carotene in an organism and thereby alter the nutritional value, pharmacology and visual appearance value of the organism. In addition, the transformed organism can be used in the formulation of therapeutic agents, for example in the treatment of cancer (see Mayne et al (1996) FASEB J. 10:690-701; Tsushima et al (1995) Biol. Pharm. Bull. 18:227-233).

An antisense strand of a nucleic acid of the invention can be inserted into a vector. For example, the lycopene ϵ -cyclase gene can be inserted into a vector and incorporated into the genomic DNA of a host, thereby inhibiting the synthesis of ϵ, β -carotenoids (lutein and α -carotene) and enhancing the synthesis of β, β -carotenoids (zeaxanthin and β -carotene).

The present invention also relates to novel enzymes which are encoded by the amino acid sequences of the invention, or portions thereof.

The present invention also relates to novel enzymes which can transform known carotenoids into novel or uncommon products. Currently ϵ -carotene (see Figure 2) and γ -carotene are commonly produced only in minor amounts. As described below, an enzyme can be produced which transforms lycopene to γ -carotene and lycopene to ϵ -carotene. With these products in hand, bulk synthesis of other carotenoids derived from them are possible. For example, ϵ -carotene can be hydroxylated to form lactucaxanthin, an isomer of lutein (one ϵ and one β ring) and zeaxanthin (two β rings) where both endgroups are, instead, ϵ rings.

In addition to novel enzymes produced by truncating the 5' region of known enzymes, as discussed above, novel enzymes which can participate in the formation of unusual carotenoids can be formed by replacing portions of one gene with an analogous sequence from a structurally related gene. For example, β -cyclase and ϵ -cyclase are structurally related (see Figure 13). By replacing a portion of β -lycopene cyclase with the analogous portion of ϵ -cyclase, an enzyme which produces γ -carotene will be produced (one β endgroup). Further, by replacing a portion of the lycopene ϵ -cyclase with the analogous portion of β -cyclase, an enzyme which produces ϵ -carotene will be produced (with some exceptions, such as the lettuce ϵ -cyclase, plant ϵ -cyclases normally produce a compound with one ϵ -endgroup, δ -carotene). Similarly, β -hydroxylase could be modified to produce enzymes of novel function by creation of hybrids with ϵ -hydroxylase.

Host systems according to the present invention can comprise any organism that already produces carotenoids or which has been genetically modified to produce carotenoids.

The IPP isomerase genes are more broadly applicable for enhancing production of any product dependent on DMAPP and/or IPP as a precursor.

Organisms which already produce carotenoids include plants, algae, some yeasts, fungi and cyanobacteria and other photosynthetic bacteria. Transformation of these hosts with vectors according to the present invention can be done using standard techniques such as those described in Misawa et al., (1990) supra; Hundle et al., (1993) supra; Hundle et al., (1991) supra; Misawa et al., (1991) supra; Sandmann et al., supra; and Schnurr et al., supra.

Transgenic organisms can be constructed which include the nucleic acid sequences of the present invention (Bird et al, 1991; Bramley et al, 1992; Misawa et al, 1994a; Misawa et al, 1994b; Cunningham et al, 1993). The incorporation of these sequences can allow the controlling of carotenoid biosynthesis, content, or composition in the host cell. These transgenic systems can be constructed to incorporate sequences which allow for the overexpression of the nucleic acids of the present invention. Transgenic systems can also be constructed containing antisense expression of the nucleic acid sequences of the present invention. Such antisense expression would result in the accumulation of the substrates of the substrates of the enzyme encoded by the sense strand.

A method for screening for eukaryotic genes which encode enzymes involved in carotenoid biosynthesis comprises transforming a prokaryotic host with a nucleic acid which may contain a eukaryotic or prokaryotic carotenoid biosynthetic gene; culturing said transformed host to obtain colonies; and screening for colonies exhibiting a different color than colonies of the untransformed host.

Suitable hosts include *E. coli*, cyanobacteria such as *Synechococcus* and *Synechocystis*, alga and plant cells. *E. coli* are preferred.

In a preferred embodiment, the above "color complementation" screening protocol can be enhanced by using mutants which are either (1) deficient in at least one carotenoid biosynthetic gene or (2) overexpress at least one carotenoid biosynthetic gene. In either case, such mutants will accumulate carotenoid precursors.

Prokaryotic and eukaryotic DNA or cDNA libraries can be screened in total for the presence of genes of carotenoid biosynthesis, metabolism and degradation. Preferred organisms to be screened include photosynthetic organisms.

E. coli can be transformed with these eukaryotic cDNA libraries using conventional methods such as those described in Sambrook et al, 1989 and according to protocols described by the vendors of the cloning vectors.

For example, the cDNA libraries in bacteriophage vectors such as lambdaZAP (Stratagene) or lambda ZIPLOX (Gibco BRL) can be excised en masse and used to transform *E. coli*.

Transformed *E. coli* can be cultured using conventional techniques. The culture broth preferably contains antibiotics to select and maintain plasmids. Suitable antibiotics include penicillin, ampicillin, chloramphenicol, etc. Culturing is typically conducted at 15-40°C, preferably at room temperature or slightly above (18-28°C), for 12 hours to 7 days.

Cultures are plated and the plates are screened visually for colonies with a different color than the colonies of the host *E. coli* transformed with the empty plasmid cloning vector. For example, *E. coli* transformed with the plasmid, pAC-BETA (described below), produce yellow colonies that accumulate β -carotene. After transformation with a cDNA library, colonies which contain a different hue than those formed by *E. coli*/pAC-BETA would be expected to contain enzymes which modify the structure or accumulation of β -carotene. Similar *E. coli* strains can be engineered which accumulate earlier products in carotenoid biosynthesis, such as lycopene, γ -carotene, etc.

Having generally described this invention, a further understanding can be obtained by reference to certain specific examples which are provided herein for purposes of illustration only and are not intended to be limiting unless otherwise specified.

EXAMPLE

I. Isolation of β -carotene hydroxylase

Plasmid Construction

An 8.6kb BglII fragment containing the carotenoid biosynthetic genes of *Erwinia herbicola* was first cloned in the BamHI site of plasmid vector pACYC184 (chloramphenicol resistant), and then a 1.1kb BamHI fragment containing the *E. herbicola* β -carotene hydroxylase (*CrtZ*) was deleted. *E. coli* strains containing the resulting plasmid, pAC-BETA, accumulate β -carotene and form yellow colonies (Cunningham et al., 1994).

A full length cDNA encoding IPP isomerase of *Haematococcus pluvialis* (HP04) was first excised with *BamHI* and *KpnI* from pBluescript SK-, and then ligated into the

corresponding sites of the pTrcHisA vector with high-level expression from the *trc* promoter (Invitrogen, Inc.). A fragment containing the IPP isomerase and *trc* promoter was subsequently excised with *EcoRV* and *KpnI*, treated with the Klenow fragment of DNA polymerase to produce blunt ends, and ligated in the Klenow-treated *HindIII* site of pAC-BETA. *E.coli* cells transformed with this new plasmid pAC-BETA-04 form orange colonies on LB plates (vs. yellow for those containing pAC-BETA) and cultures accumulate substantially more β -carotene (ca. two fold) than those that contain pAC-BETA.

Screening of an Arabidopsis cDNA Library

Several λ cDNA expression libraries of *Arabidopsis* were obtained from the *Arabidopsis* Biological Resource Center (Ohio State University, Columbus, OH) (Kieber et al., 1993). The λ cDNA libraries were excised *in vivo* using Stratagene's ExAssist SOLR system to produce a phagemid cDNA library wherein each phagemid contained also a gene conferring resistance to the antibiotic ampicillin.

E.coli strain DH10BZIP was chosen as the host cell for the screening and pigment production, although we have also used TOP10F' and XL1-Blue for this purpose. DH10B cells were transformed with plasmid pAC-BETA-04 and were plated on LB agar plates containing chloramphenicol at 50 μ g/ml (from United States Biochemical Corporation). The phagemid *Arabidopsis* cDNA library was then introduced into DH10B cells already containing pAC-BETA-04. Transformed cells containing both pAC-BETA-04 and *Arabidopsis* cDNA library phagemids were selected on chloramphenicol plus ampicillin (150 μ g/ml) agar plates. Maximum color development occurred after 3 to 7 days incubation at room temperature, and the rare bright yellow colonies were selected from a background of many thousands of orange colonies on each agar plate. Selected colonies were inoculated into 3 ml liquid LB medium containing ampicillin and chloramphenicol, and cultures were incubated at room temperature for 1-2 days, with shaking. Cells were then harvested by centrifugation and extracted with acetone in microfuge tubes. After centrifugation, the pigmented extract was spotted onto silica gel thin-layer chromatography (TLC) plates, and developed with a hexane:ether (1:1, by volume) mobile phases. β -carotene hydroxylase-encoding cDNAs were identified based on the appearance of a yellow pigment that co-migrated with zeaxanthin on the TLC plates.

Subcloning and Sequencing

The plasmid containing the β -carotene hydroxylase cDNA was recovered and analyzed by standard procedures (Sambrook et al., 1989). The *Arabidopsis* β -carotene hydroxylase was sequenced completely on both strands on an automatic sequencer (Applied Biosystems, Model 373A, Version 2.0.1S). The cDNA insert of 0.95kb also was excised and ligated into the a pTrcHis vector. A *Bgl*II restriction site within the cDNA was used to remove that portion of the cDNA that encodes the predicted polypeptide N terminal sequence region that is not also found in bacterial β -carotene hydroxylases (Figure 6). A *Bgl*II-*Xho*I fragment was directionally cloned in BamHI-*Xho*I digested TrcHis vectors.

Pigment Analysis

A single colony was used to inoculate 50 ml of LB containing ampicillin and chloramphenicol in a 250-ml flask. Cultures were incubated at 28°C for 36 hours with gentle shaking, and then harvested at 5000 rpm in an SS-34 rotor. The cells were washed once with distilled H₂O and resuspended with 0.5 ml of water. The extraction procedures and HPLC were essentially as described previously (Cunningham et al, 1994).

II. Isolation and biochemical analysis of an Arabidopsis lycopene ϵ -cyclase

Plasmid Construction

Construction of plasmids pAC-LYC, pAC-NEUR, and pAC-ZETA is described in Cunningham et al., (1994). In brief, the appropriate carotenoid biosynthetic genes from *Erwinia herbicola*, *Rhodobacter capsulatus*, and *Synechococcus* sp. strain PCC7942 were cloned in the plasmid vector pACYC184 (New England BioLabs, Beverly, MA). Cultures of *E. coli* containing the plasmids pAC-ZETA, pAC-NEUR, and pAC-LYC, accumulate ζ -carotene, neurosporene, and lycopene, respectively. The plasmid pAC-ZETA was constructed as follows: an 8.6-kb *Bgl*II fragment containing the carotenoid biosynthetic genes of *E. herbicola* (GenBank M87280; Hundle et al., 1991) was obtained after partial digestion of plasmid pPL376 (Perry et al., 1986; Tuveson et al., 1986) and cloned in the BamHI site of pACYC184 to give the plasmid pAC-EHER. Deletion of adjacent 0.8- and 1.1-kb BamHI-BamHI fragments (deletion Z in Cunningham et al., 1994), and of a 1.1 kB *Sall*-*Sall* fragment (deletion X) served to remove most of the coding regions for the *E. herbicola* β -carotene hydroxylase (*crtZ* gene) and zeaxanthin glucosyltransferase (*crtX* gene), respectively. The

resulting plasmid, pAC-BETA, retains functional genes for geranylgeranyl pyrophosphate synthase (crtE), phytoene synthase (crtB), phytoene desaturase (crtI), and lycopene cyclase (crtY). Cells of *E. coli* containing this plasmid form yellow colonies and accumulate β -carotene. A plasmid containing both the lycopene ϵ - and β -cyclase cDNAs of *A. thaliana* was constructed by excising the ϵ -cyclase in clone y2 as a PvuI-PvuII fragment and ligating this piece in the SnaBI site of a plasmid (pSPORT 1 from GIBCO-BRL) that already contained the β -cyclase (Cunningham et al., 1996).

Organisms and Growth Conditions

E. coli strains TOP10 and TOP10 F' (obtained from Invitrogen Corporation, San Diego, CA) and XL1-Blue (Stratagene) were grown in Luria-Bertani (LB) medium (Sambrook et al., 1989) at 37°C in darkness on a platform shaker at 225 cycles per min. Media components were from Difco (yeast extract and tryptone) or Sigma (NaCl). Ampicillin at 150 μ g/mL and/or chloramphenicol at 50 μ g/mL (both from United States Biochemical Corporation) were used, as appropriate, for selection and maintenance of plasmids.

Mass Excision and Color Complementation Screening of an *A. thaliana* cDNA Library

A size-fractionated 1-2 kB cDNA library of *A. thaliana* in lambda ZAPII (Kieber et al., 1993) was obtained from the Arabidopsis Biological Resource Center at The Ohio State University (stock number CD4-14). Other size fractionated libraries were also obtained (stock numbers CD4-13, CD4-15, and CD4-16). An aliquot of each library was treated to cause a mass excision of the cDNAs and thereby produce a phagemid library according to the instructions provided by the supplier of the cloning vector (Stratagene; *E. coli* strain XL1-Blue and the helper phage R408 were used). The titre of the excised phagemid was determined and the library was introduced into a lycopene-accumulating strain of *E. coli* TOP10 F' (this strain contained the plasmid pAC-LYC) by incubation of the phagemid with the *E. coli* cells for 15 min at 37°C. Cells had been grown overnight at 30°C in LB medium supplemented with 2% (w/v) maltose and 10 mM MgSO₄ (final concentration), and harvested in 1.5 ml microfuge tubes at a setting of 3 on an Eppendorf microfuge (5415C) for 10 min. The pellets were resuspended in 10 mM MgSO₄ to a volume equal to one-half that of the

initial culture volume. Transformants were spread on large (150 mm diameter) LB agar petri plates containing antibiotics to provide for selection of cDNA clones (ampicillin) and maintenance of pAC-LYC (chloramphenicol). Approximately 10,000 colony forming units were spread on each plate. Petri plates were incubated at 37°C for 16 hr and then at room temperature for 2 to 7 days to allow maximum color development. Plates were screened visually with the aid of an illuminated 3x magnifier and a low power stage-dissecting microscope for the rare, pale pinkish-yellow to deep-yellow colonies that could be observed in the background of pink colonies. A colony color of yellow or pinkish-yellow was taken as presumptive evidence of a cyclization activity. These yellow colonies were collected with sterile toothpicks and used to inoculate 3ml of LB medium in culture tubes with overnight growth at 37°C and shaking at 225 cycles/min. Cultures were split into two aliquots in microfuge tubes and harvested by centrifugation at a setting of 5 in an Eppendorf 5415C microfuge. After discarding the liquid, one pellet was frozen for later purification of plasmid DNA. To the second pellet was added 1.5 ml EtOH, and the pellet was resuspended by vortex mixing, and extraction was allowed to proceed in the dark for 15-30 min with occasional remixing. Insoluble materials were pelleted by centrifugation at maximum speed for 10 min in a microfuge. Absorption spectra of the supernatant fluids were recorded from 350-550 nm with a Perkin Elmer lambda six spectrophotometer.

Analysis of isolated clones

Eight of the yellow colonies contained β -carotene indicating that a single gene product catalyzes both cyclizations required to form the two β endgroups of the symmetrical β -carotene from the symmetrical precursor lycopene. One of the yellow colonies contained a pigment with the spectrum characteristic of δ -carotene, a monocyclic carotenoid with a single ϵ endgroup. Unlike the β cyclase, this ϵ -cyclase appears unable to carry out a second cyclization at the other end of the molecule.

The observation that ϵ -cyclase is unable to form two cyclic ϵ -endgroups (e.g. the bicyclic ϵ -carotene) illuminates the mechanism by which plants can coordinate and control the flow of substrate into carotenoids derived from β -carotene versus those derived from α -carotene and also can prevent the formation of carotenoids with two ϵ endgroups.

The availability of the *A. thaliana* gene encoding the ϵ -cyclase enables the directed manipulation of plant and algal species for modification of carotenoid content and

composition. Through inactivation of the ϵ -cyclase, whether at the gene level by deletion of the gene or by insertional inactivation or by reduction of the amount of enzyme formed (by such as antisense technology), one may increase the formation of β -carotene and other pigments derived from it. Since vitamin A is derived only from carotenoids with β endgroups, an enhancement of the production of β -carotene versus α -carotene may enhance nutritional value of crop plants. Reduction of carotenoids with ϵ -endgroups may also be of value in modifying the color properties of crop plants and specific tissues of these plants. Alternatively, where production of α -carotene, or pigments such as lutein that are derived from α -carotene, is desirable, whether for the color properties, nutritional value or other reason, one may overexpress the ϵ -cyclase or express it in specific tissues. Wherever agronomic value of a crop is related to pigmentation provided by carotenoid pigments the directed manipulation of expression of the ϵ -cyclase gene and/or production of the enzyme may be of commercial value.

The predicted amino acid sequence of the *A. thaliana* ϵ -cyclase enzyme was determined. A comparison of the amino acid sequences of the β - and ϵ -cyclase enzymes of *Arabidopsis thaliana* (Fig. 13) as predicted by the DNA sequence of the respective cDNAs (Fig. 4 for the ϵ -cyclase cDNA sequence), indicates that these two enzymes have many regions of sequence similarity, but they are only about 37% identical overall at the amino acid level. The degree of sequence identity at the DNA base level, only about 50%, is sufficiently low such that we and others have been unable to detect this gene by hybridization using the β cyclase as a probe in DNA gel blot experiments.

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- 30 Having now fully described the invention, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the invention as set forth herein.

We claim:

1. An isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase enzyme activity and has an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23 or 25-27.
- 5 2. The nucleic acid sequence of claim 1, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23 or 25-27.
3. A vector comprising the nucleic acid sequence of claim 1, wherein the nucleic acid sequence is operably linked to a promoter.
4. A host cell which contains the vector of claim 3.
- 10 5. The host cell of claim 4, wherein the host cell is selected from the group consisting of a bacterial cell, an algal cell, a yeast cell and a plant cell.
6. The host cell of claim 4, wherein the host cell is a photosynthetic cell.
7. An isolated and/or purified protein having lycopene ϵ -cyclase enzyme activity and having an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23 or
15 25-27.
8. The protein of claim 7, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23 or 25-27.

AMENDED CLAIMS

[received by the International Bureau on 15 November 1999 (15.11.99);
original claims 1,2,7 and 8 amended; remaining claims unchanged (1 page)]

1. An isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ -cyclase enzyme activity and has an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23, 25 or 26.
- 5 2. The nucleic acid sequence of claim 1, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23, 25 or 26.
3. A vector comprising the nucleic acid sequence of claim 1, wherein the nucleic acid sequence is operably linked to a promoter.
4. A host cell which contains the vector of claim 3.
- 10 5. The host cell of claim 4, wherein the host cell is selected from the group consisting of a bacterial cell, an algal cell, a yeast cell and a plant cell.
6. The host cell of claim 4, wherein the host cell is a photosynthetic cell.
7. An isolated and/or purified protein having lycopene ϵ -cyclase enzyme activity and having an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23, 25
15 or 26.
8. The protein of claim 7, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23, 25 or 26.

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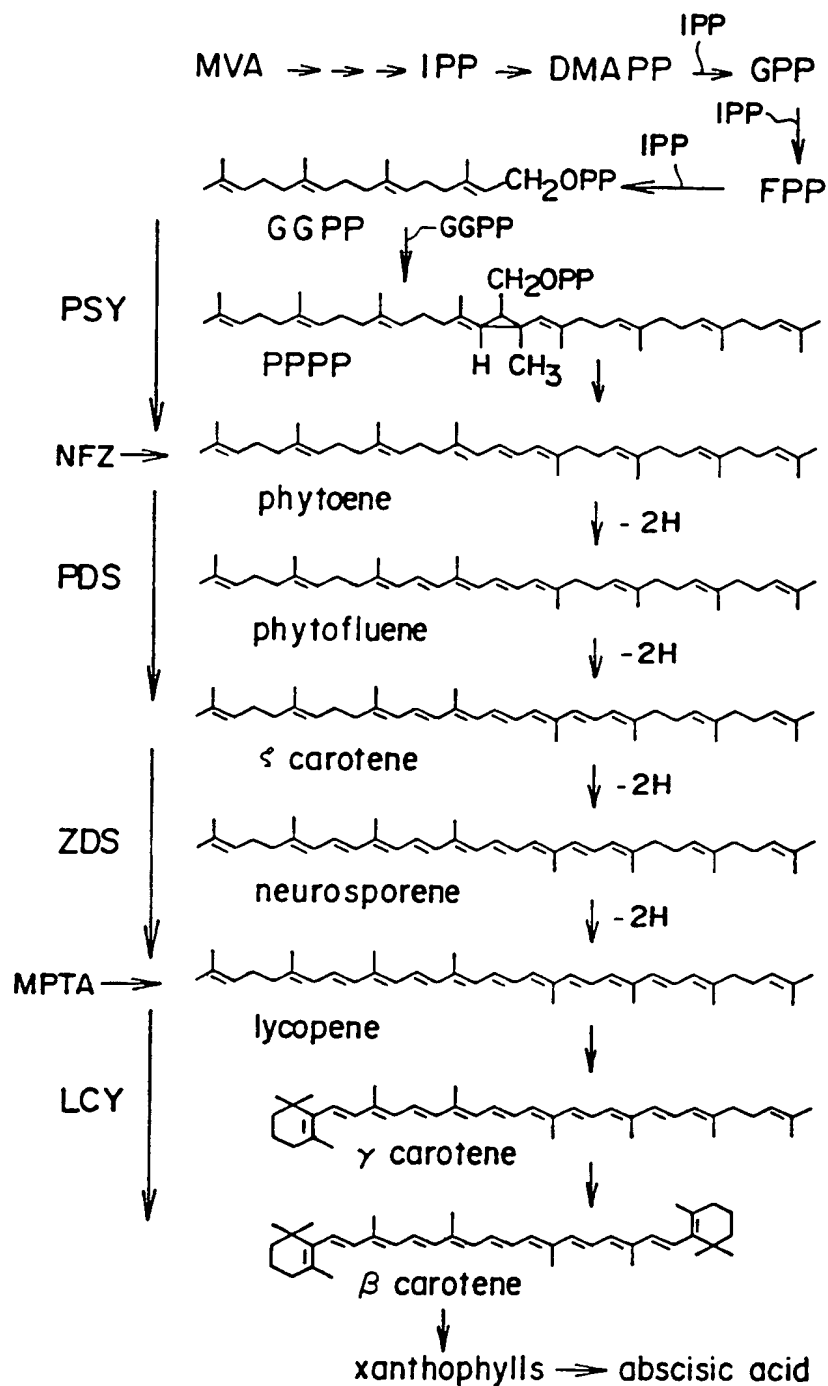
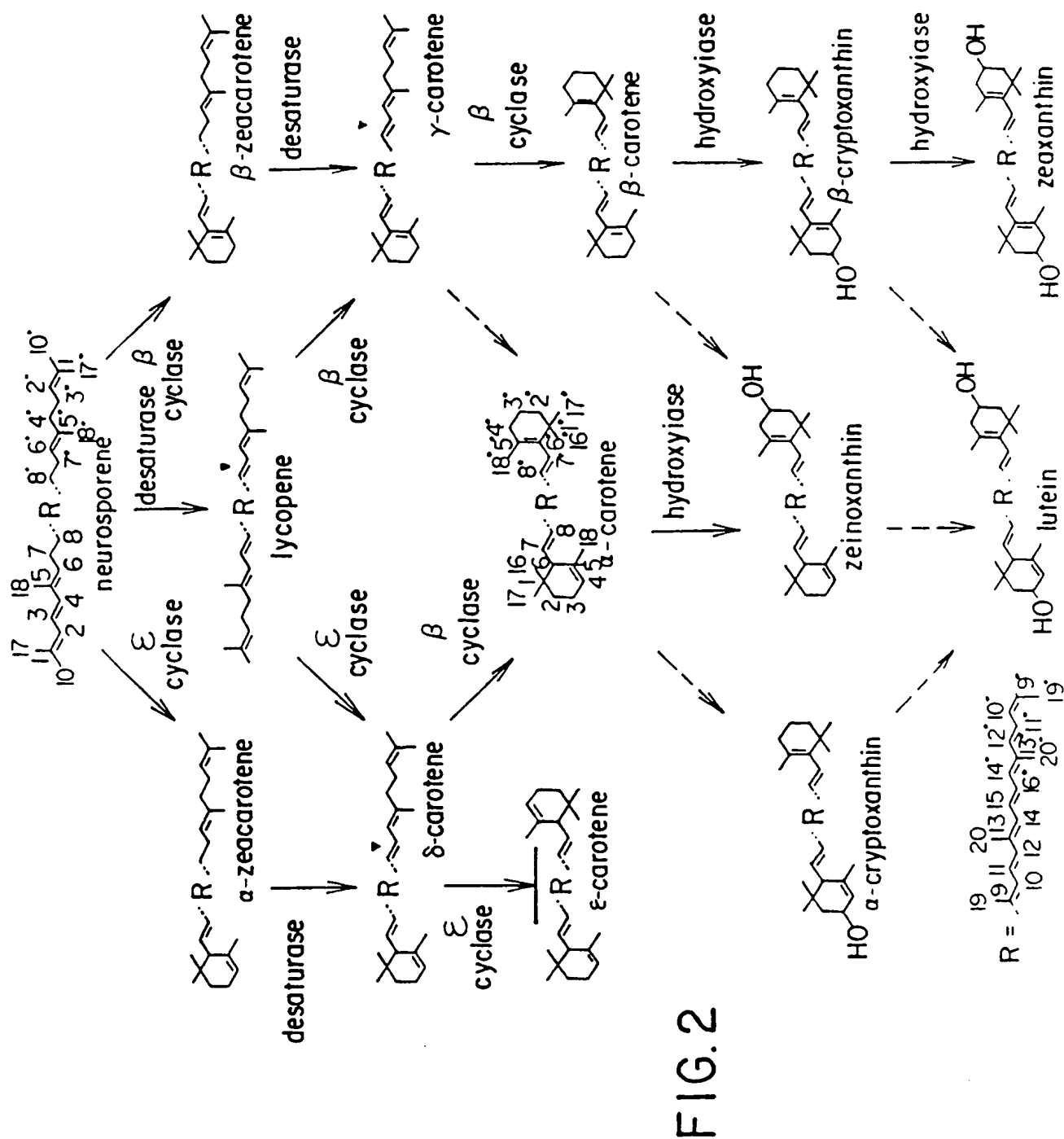
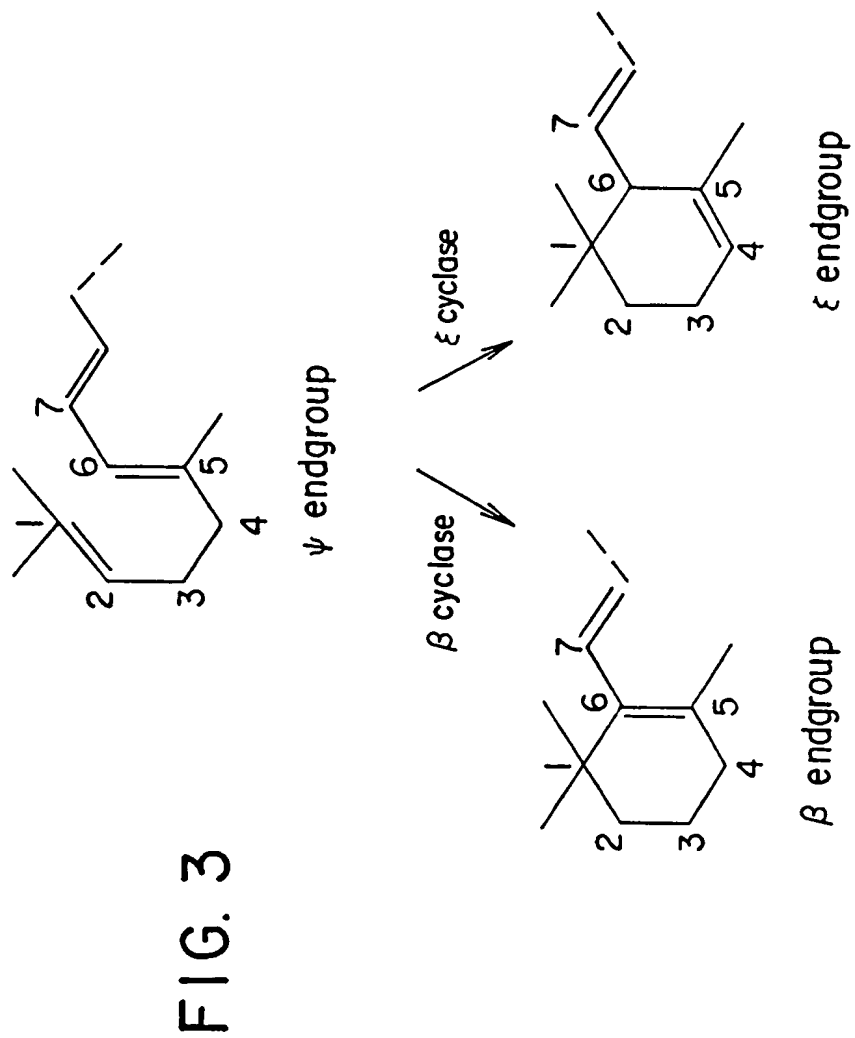


FIG. 1



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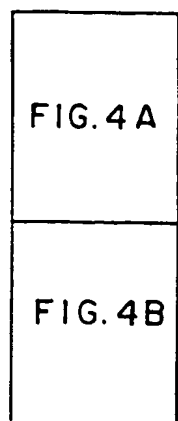


FIG. 4

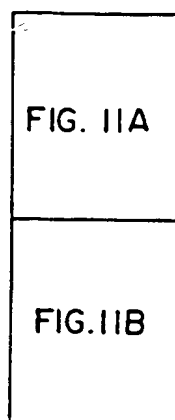


FIG. II

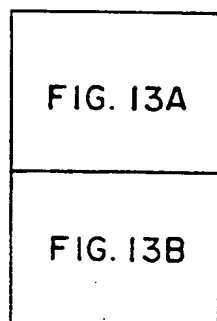


FIG. 13

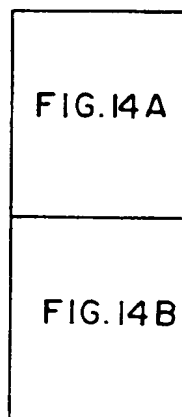


FIG. 14

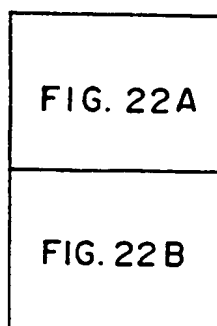


FIG. 22

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FIG. 4A

Arabidopsis thaliana epsilon cyclase:

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          acaaaaggaaataattag attcctctttctgcttgctataccttgaca 48
gaacaacataacaatggtgtaagtcttctc gctgtattcgaaattatttggaggaggaaac 108
atggagtgtgttgggctaggaatttcgca gcaatggcggtttcaacatttccgtcatgg 168
1  M E C V G A R N F A A M A V S T F P S W
agttgtcgaaggaaatttccagtggctaag agatacagctataggaatattcgttcggt 228
21 S C R R K F P V V K R Y S Y R N I R F G
ttgtgtagtgtcagagctagcggcgggcga agttccggtagtgagagttgtgtagcgggtg 288
41 L C S V R A S G G G S S G S K S C V A V
agagaagatttgcgtgacgaagaagatttt gcgaaagctggcggttctgagattctattt 348
61 R S D F A D E E D F V E A G G S R I L F
gttcaaatgcagcagaacaaagatatggat gaacagtctaagcttgttgataagttgcct 408
81 V Q M Q Q M K D M D S Q S K L V D K L P
cctatatcaactggtgatggtgctttggat catgtggttactggctgtggtcctgctggt 468
101 P I S I G D G A L D K V V I G C G P A G
ttagccttggctgcagaatcagctaagctt ggattaaaagttggactcattggtccagat 528
121 L A L A A K S A K L G L K V G L I G P D
cttccttttactaacaattacggtgtttgg gaagatgaattcaatgatcttgggctgcaa 588
141 L P F T M M Y G V M K D K F N D L G L G
aaatgtattgagcatgtttggagagagact attgcgcacctggatgatgacaagcctatt 648
161 K C I K K V W R S T I V Y L D D D K P I
accattggccgtgcttatggaagagttagt cgacgtttgctccatgaggagcttttgagg 708
181 T I G R A Y G R V S R R L L X E E L L R
aggtgtgtcgagtcaggtgtctcgctacctt agctcgaaagttgacagcataacagaagct 768
201 R C V K S G V S Y L S S K V D S I T E A
tgtgatggccttagacttgttgcttgtgac gacaataacgtcattccctgcaggcttgcc 828
221 S D G L X L V A C D D M M V I P C X L A
actgttgcttctggagcagcttcgggaaag ctcttgcaatacgaagttggtggacctaga 888
241 T V A S G A A S G K L L Q Y X V G G P R
gtctgtgcgcaaactgcatacggcgtggag gttgaggcggaataagtcctatgatcca 948

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FIG. 4B

261 V C V Q T A Y G V X V X V X N S P Y D P
 gatcaaatggttttcatggattacagagat tataactaacgagaaagttcggagcttagaa 1008
 281 D Q M V P M D Y R D Y T M X X V R S L X
 gctgagtatccaacgtttctgtacgccatg cctatgacaaagtcaagactcttcttcgag 1068
 301 A K Y P T F L Y A M P M T K S R L F F K
 gagacatgtttggcctcaaaagatgtcatg ccctttgatttgctaaaaacgaagctcatg 1128
 321 K T C L A S K D V M P F D L L K T K L M
 ttaagattagacacactcggaaattcgaatt ctaaagacttacgaagaggagtggctctat 1188
 341 I P V G G S L P N T X Q K N L A F G A A
 atcccagttggtggttccttgccaaacacc gaacaaaagaatctcgcctttggtgctgcc 1248
 361 I P V G G S L P M T X Q K N L A F G A A
 gctagcatggtacatcccgaacaggctat tcagttgtgagatctttgtctgaagctcca 1308
 381 A S M V M P A T G Y S V V R S L S X A P
 aaacatgcatcagtcacgcagagatacta agagaagagactaccaaacagattaacagt 1368
 401 K Y A S V I A K I L R E E T T K Q I N S
 aatatttcaagacaagcttaggatacttta tggccaccagaaaggaaaagacagagagca 1428
 421 M I S R Q A W D T L W P P E R X R Q R A
 ttctttctctttggtcttgcaactcagagtt caattcgataccgaaggcattagaagcttc 1488
 441 F F L F G L A L I V Q F D T X G I R S F
 ttccgtactttcttccgccttccaaaatgg atgtggcaagggtttctaggatcaacatta 1548
 461 F R T P F R L P K W M W Q G F L G S T L
 acatcaggagatctcgttctctttgcttta tacatgttcgtcatttcaccaaacaatttg 1608
 481 T S G D L V L F A L Y M P V I S P M M L
 agaaaaggtctcattaatcatctcatctct gatccaaccggagcaaccatgataaaaacc 1668
 501 R K G L I N W L I S D P T G A T M I K T
 tatctcaaagtatgatttacttaccaactc ttaggtttgtgtatatatatgccgatttat 1728
 521 Y L K V
 ctgaataatcgatcaaagaatggtatgtgg gttactaggaagttggaaacaaacacgtat 1788
 agaatctaaggagtgatcgaaatggagacg gaaacgaaaagaaaaaatcagtcctttgtt 1848
 ccgtggctagtg 1868

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FIG. 5

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1  gctctttctc ctccctctct accgatttcc gactccgcct cccgaaatcc
51  ttatccggat tctctccgtc tcttcgattt aaacgccttt ctgtctgtta
101 cgtcgtcgaa gaacggagac agaattctcc gattgagaac gatgagagac
151 cggagagcac gagctccaca aacgctatag acgctgagta tctggcgttg
201 cgtttgccgg agaaattgga gaggaagaaa tcggagaggt ccacttatct
251 aatcgctgct atgttgctga gctttggtat cacttctatg gctgttatgg
301 ctgtttacta cagattctct tggcaaattg agggaggtga gatctcaatg
351 ttggaatgtt ttggtacatt tgctctctct gttggtgctg ctgttggtat
401 ggaattctgg gcaagatggg ctcatagagc tctgtggcac gcttctctat
451 ggaatatgca tgagtcacat cacaaccaa gagaaggacc gtttgagcta
501 aacgatgttt ttgctatagt gaacgctggg ccagcgattg gtctcctctc
551 ttatggattc ttcaataaag gactcgttcc tgggtctctgc tttggcgccg
601 ggttaggcat aacggtgttt ggaatcgctt acatgtttgt ccacgatggt
651 ctcgctgcaca agcggttccc tgtaggtccc atcgccgacg tcccttacct
701 ccgaaaggct gccgccgctc accagctaca tcacacagac aagttcaatg
751 gtgtaccata tggactgttt cttggacca aggaattgga agaagttgga
801 ggaaatgaag agttagataa ggagattagt cggagaatca aatcatacaa
851 aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt
901 ttaaatccca aattcttttt ttgtcttctg tcattatgat catcttaaga
951 cggtct
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FIG. 6

A.thal.	SFSS SSTDFRLRLP KSLSGFSPSL RFRKFSVCYV VEERRONSPI ENDERPESTS STNAIDAEYL	64
A.thal.	ALRLAEKLER KKSERSTYLI AAMLSSFGIT SMAVMVYR FSNQMEGGEI SMLEMFGTFA LSVGAAGVME FWAQWAHRAAL	144
A.alcal.
A.aurant.
E.herb.
E.ured.
Consensus	-----f- --v-----ME --A---Hr--	
<hr/>		
	Predicted TM helix	Predicted TM helix
A.thal.	WNASL.MNMH ESHHKPREGP FELNDVFAIV NAGPATGILLS YGFENKGLVP GLCFGAGLGI TVFGIAYMFV HDGLVHKRFP	224
A.alcal.	MGPLGAGMH KSHHEHDHA LEKNDLYGW FAVLATILFT VGAYMWPVLW WI....ALGM TVYGLIYFIL HDGLVHORWP	
A.aurant.	MGPLGAGMH KSHHEHDHA LEKNDLYGLV FAVIATVLEF VGTIAPVLW WI....ALGM TVYGLIYFVL HDGLVHORWP	
E.herb.	MHG.WGWRWH ESHHTPRKGV FKNDLFAW FAGVAIALIA VGTAGWPLO WI....GCCM TVYGLLYFLV HDGLVHORWP	
E.ured.	MHG.WGWRWH LSHHEPRKGA FEVNDLYAW FAALSILLIY LGSTGMWPLQ WI....GAGM TAYGLLYFMV HDGLVHORWP	
Consensus	-H--l-W--H -SHH-pr-g- fE-ND--a-v -A--ai-L-- -G-----glG- Tv-G--Y--v HDGLVH-R-P	
<hr/>		
	Predicted TM helix	Predicted TM helix
A.thal.	VGPIADVPYL RKVAAAHQLH HT..DKFNGV PYGLFLGPKE LEEVGGNEEL DKEISRRIKS YKKASGSGSS SSS*...	301
A.alcal.	FRYIPRRGYF RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKODLKR SGVLRPODER PS*.....	
A.aurant.	FRYIPRKGYA RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKODLKM SGVLRPAEOE RT*.....	
E.herb.	FHWIPRRGYL KRLYVAHRLH HAVRGREGCV SFGFIYARK. PADLOAILRE RHGRPPKRDA AKORPDAASP SSSSPE*	
E.ured.	FRYIPRKGYL KRLYMAHRLH HAVRGKEGCV SFGFIYAPP. LSKLOATLRE RHG..ARAGA ARDAQGEDE PASGK*.	
Consensus	---I-----YI r-----AH-1H H-----V --G-----p-- -----S-----	

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FIG. 7

1 ccacgggtcc gcctccccgt ttttttccga tccgatctcc ggtgccgagg
51 actcagctgt ttgttcgctc tttctcagcc gtcaccatga ccgattctaa
101 cgatgctgga atggatgctg ttcagagacg actcatgttt gaagacgaat
151 gcattctcgt tgatgaaaaat aatcgtgtgg tgggacatga cactaagtat
201 aactgtcatc tgatggaaaa gattgaagct gagaatttac ttcacagagc
251 tttcagtgtg tttttattca actccaagta tgagttgctt ctccagcaac
301 ggtcaaaaac aaagggttact ttcccacttg tgtggacaaa cacttggtgc
351 agccatcctc tttaccgtga atccgagctt attgaagaga atgtgcttgg
401 tgtaagaaat gccgcacaaa ggaagctttt cgatgagctc ggtattgtag
451 cagaagatgt accagtcgat gagttcactc ccttgggacg catgctttac
501 aaggcacctt ctgatgggaa atggggagag cacgaagttg actatctact
551 cttcatcgtg cgggatgtga agcttcaacc aaaccagat gaagtggctg
601 agatcaagta cgtgagcagg gaagagctta aggagctggt gaagaaagca
651 gatgctggcg atgaagctgt gaaactatct ccatggttca gattggtggt
701 ggataatttc ttgatgaagt ggtgggatca tgttgagaaa ggaactatca
751 ctgaagctgc agacatgaaa accattcaca agctctgaac tttccataag
801 ttttggatct tccccctccc ataataaaat taagagatga gacttttatt
851 gattacagac aaaactggca acaaaatcta ttcctaggat ttttttttgc
901 tttttattta cttttgatcc atctctagtt tagttttcat cttaaaaaaa
951 aaaa

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FIG. 8

1 caccaatgtc tgtttcttct ttatttaatc tcccattgat tcgcctcaga
51 tctctcgcgc tttcgtcttc tttttcttct ttccgatttg cccatcgctc
101 TCTGTCATCG ATTTCAACCGA GAAAGTTACC GAATTTTCGT GCTTTCTCTG
151 GTACCGCTAT GACAGATACT AAAGATGCTG GTATGGATGC TGTTCAGAGA
201 CGTCTCATGT TTGAGGATGA ATGCATTCTT GTTGATGAAA CTGATCGTGT
251 TGTGGGGCAT GTCAGCAAGT ATAATTGTCA TCTGATGGAA AATATTGAAG
301 CCAAGAATTT GCTGCACAGG GCTTTTAGTG TATTTTATT CAACTCGAAG
351 TATGAGTTGC TTCTCCAGCA AAGGTCAAAC ACAAAGGTTA CGTTCCCTCT
401 AGTGTGGACT AACACTTGTT GCAGCCATCC TCTTTACCGT GAATCAGAGC
451 TTATCCAGGA CAATGCACTA GGTGTGAGGA ATGCTGCACA AAGAAAGCTT
501 CTCGATGAGC TTGGTATTGT AGCTGAAGAT GTACCAGTCG ATGAGTTCAC
551 TCCCTTGGA CGTATGCTGT ACAAGGCTCC TTCTGATGGC AAATGGGGAG
601 AGCATGAACT TGATTACTTG CTCTTCATCG TGCGAGACCT GAAGGTTCAA
651 CCAAACCCAG ATGAAGTAGC TGAGATCAAG TATGTGAGCC GGAAGAGCT
701 GAAGGAGCTG GTGAAGAAAG CAGATGCAGG TGAGGAAGGT TTGAACTGT
751 CACCATGGTT CAGATTGGTG GTGGACAATT TCTTGATGAA GTGGTGGGAT
801 CATGTTGAGA AAGGAACTTT GGTGAAGCT ATAGACATGA AAACCATCCA
851 CAACTCTGA ACATCTTTT TTAAAGTTT TAAATCAATC AACTTTCTCT
901 TCATCATTTT TATCTTTTCG ATGATAATAA TTTGGGATAT GTGAGACACT
951 TACAAAACCT CCAAGCACCT CAGGCAATAA TAAAGTTTGC GGCCGC

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FIG. 9

1 CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCG GCGGCAGTCC
51 GATGCCGCGA TGCTTCGTTC GTTGCTCAGA GGCCTCACGC ATATCCCCCG
101 CGTGAACCTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA
151 AGCTCAGGAG CATGCAGATG ACGCTCATGC AGCCCAGCAT CTCAGCCAAT
201 CTGTGCGCGG CCGAGGACCG CACAGACCAC ATGAGGGGTG CAAGCACCTG
251 GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT
301 TGGTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGATGT
351 CACAAGTTCC TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC
401 TGTGTTCTTG TTTGACGATC AGGGGCGACT GCTGCTGCAA CAGCGTGCAC
451 GCTCAAAAAT CACCTTCCCA AGTGTGTGGA CGAACACCTG CTGCAGCCAC
501 CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA GCCAGGTGGC
551 CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC
601 ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC
651 CTCACGCGTT TGCCTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA
701 ATCAGCGCTC TGGGGCGAGC ACGAAATGGA CTACATCTTG TTCATCCGGG
751 CCAACGTCAC CTTGGCGCCC AACCCTGACG AGGTGGACGA AGTCAGGTAC
801 GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA ACGGGCTGCA
851 ATGGTCGCGG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT
901 GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA
951 ACGGTGCATC ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA
1001 GACACGTCAT GGGGTGGAAT TCGTACTTG GCAGCTTCGT ATCTCCTTTT
1051 TCTGAGACTG AACCTGCAGT CAGGTCCAC AAGGTCAGGT AAAATGGCTC
1101 GATAAAATGT ACCGTCACCT TTTGTCGCGT ATACTGAACT CCAAGAGGTC
1151 AAAAAAAAAA AAAAA

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FIG. 10

1 CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCCG GCGGCAGTCC
51 GATGCCGCGA TGCTTCGTTC GTTGCTCAGA GGCCTCAGGC ATATCCCCGG
101 CGTGAAGTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA
151 AGCTCAGGAG CATGCAGCTG CTTTCCGAGG ACCGCACAGA CCACATGAGG
201 GGTGCAAGCA CCTGGGCAGG CGGGCAGTCG CAGGATGAGC TGATGCTGAA
251 GGACGAGTGC ATCTTGGTAG ATGTTGAGGA CAACATCACA GGCCATGCCA
301 GCAAGCTGGA GTGTCACAAG TTCCTACCAC ATCAGCCTGC AGGCCTGCTG
351 CACCGGGCCT TCTCTGTGTT CCTGTTTGAC GATCAGGGGC GACTGCTGCT
401 GCAACAGCGT GCACGCTCAA AAATCACCTT CCCAAGTGTG TGGACGAACA
451 CCTGCTGCAG CCACCCTTTA CATGGGCAGA CCCCAGATGA GGTGGACCAA
501 CTAAGCCAGG TGGCCGACGG AACAGTACCT GGCGCAAAGG CTGCTGCCAT
551 CCGCAAGTTG GAGCAGGAGC TGGGGATACC AGCGCACCAG CTGCCGGCAA
601 GCGCGTTTCG CTTCTCAGC CGTTTGCACT ACTGTGCCGC GGACGTGCAG
651 CCAGCTGCGA CACAATCAGC GCTCTGGGGC GAGCACGAAA TGGACTACAT
701 CTTGTTTCATC CGGGCCAACG TCACCTTGGC GCCCAACCCT GACGAGGTGG
751 ACGAAGTCAG GTACGTGACG CAAGAGGAGC TGCGGCAGAT GATGCAGCCG
801 GACAACGGGC TTCAATGGTC GCCGTGGTTT CGCATCATCG CCGCGCGCTT
851 CCTTGAGCGT TGGTGGGCTG ACCTGGACGC GGCCCTAAAC ACTGACAAAC
901 ACGAGGATTG GGGAACGGTG CATCACATCA ACGAAGCGTG AAGGCAGAAG
951 CTGCAGGATG TGAAGACACG TCATGGGGTG GAATTGCGTA CTTGGCAGCT
1001 TCGTATCTCC TTTTCTGAG ACTGAACCTG CAGAGCTAGA GTCAATGGTG
1051 CATCATATTC ATCGTCTCTC TTTTGTTTTA GACTAATCTG TAGCTAGAGT
1101 CACTGATGAA TCCTTTACAA CTTTCAAAAA AAAAA

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FIG. 11A

1					50
HPO4	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQMTLM	QPSISANLSR
HPO5	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQLL..
ATDP7	MSVSSLFNL	.LIRLRLSLA.	LSSSFSSFRF	AHRPLSSIS.	PRKLPNFRF
C.brew.	MS.SSMLNFT	.ASRIVSLPL	LSSPPSRVHL	PLCFFSPISL	TQRFSAKLTF
ATOP5TGPPPRFFP	IRSPVPRTO	FVRAFSAV..
S.cerev.	..MTADNNSM	PHGAVSSYAK	LVQNQTPEDI	LEEFPEIIP	QQRPN...TR
51					100
AEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF	
SEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF	
S..GTA.MTD	TKDAGMDAVQ	RRLMFEDECI	LVDETDRVVG	HVSKYNCHLM	
SSQATT.MGE	VVDAGMDAVQ	RRLMFEDECI	LVDENDKVVG	HESKYNCHLM	
.....T.MTD	SNDAGMDAVQ	RRLMFEDECI	LVDENNRVVG	HDTKYNCHLM	
SSETSNDESG	ETCFSGHDEE	QIKLMNENCI	VLDWDDNAIG	AGTKKVCHLM	
101					150
LPHQPAGLLH	RAFSVFLFDD	QGRLLLQORA	RSKITFPSVW	TNTCCSHPLH	
LPHQPAGLLH	RAFSVFLFDD	QGRLLLQORA	RSKITFPSVW	TNTCCSHPLH	
ENIEAKNLLH	RAFSVFLFNS	KYELLLOQRS	NTKVTFPLVW	TNTCCSHPLY	
ENIESENLLH	RAFSVFLFNS	KYELLLOQRS	ATKVTFPLVW	TNTCCSHPLY	
EKIEAENLLH	RAFSVFLFNS	KYELLLOQRS	TKKVTFPLVW	TNTCCSHPLY	
ENIE.KGLLH	RAFSVFIFNE	QGELLLOQRA	TEKITFPDLW	TNTCCSHPLC	
151					200
GQTPDEVQDL	SQVADGTVPG	AKAAAIRKLE	HELGIPAHQL	PA.SAFRFLT	
GQTPDEVQDL	SQVADGTVPG	AKAAAIRKLE	HELGIPAHQL	PA.SAFRFLT	
RE.....	SELIQDNALG	VRNAAQRKLL	DELGIVAEDV	PV.DEFTPLG	
RE.....	SELIDENCLG	VRNAAQRKLL	DELGIPAEDL	PV.DQFIPLS	
RE.....	SELIEENVLG	VRNAAQRKLF	DELGIVAEDV	PV.DEFTPLG	
ID...DELGL	KGKLDDKIKG	AITAAVRKLD	HELGIPEDET	KTRGKFHFLN	
201					250
RLHYCAADVQ	PAATQSALWG	EHEMDYILFIRANVT	APNPDEVDEV	
RLHYCAADVQ	PAATQSALWG	EHEMDYILFIRANVT	APNPDEVDEV	
RMLY.....	.KAPSDGKWG	EHELDYLLFIVRDVKV	QPNPDEVAEI	
RILY.....	.KAPSDGKWG	EHELDYLLFIIRDVNL	DPNPDEVAEV	
RMLY.....	.KAPSDGKWG	EHEVDYLLFIVRDVKL	QPNPDEVAEI	
RIHY.....	.MAPSNEPWG	EHEIDYILFY	KINAKENLTV	NPNVNEVRDF	

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FIG. 11B

251
RYVTQEELRQ MMQ....PDN GLOWSPWFRI IAARFLERWW ADLDAALNTD 300
RYVTQEELRQ MMQ....PDN GLOWSPWFRI IAARFLERWW ADLDAALNTD
KYVSREELKE LVKKADAGEE GLKLSPWFRL VVDNFLMKWW DHVEKGTLE
KYMNRDDLKE LLRKADAEED GVKLSPWFRL VVDNFLFKWW DHVEKGSLKD
KYVSREELKE LVKKADAGDE AVKLSPWFRL VVDNFLMKWW DHVEKGTITE
KWSPNDLKT MF.....ADP SYKFTPWFKI ICENYLFNWW EQDDLSEVE

301
KHEDWGTVHH INEA*
KHEDWGTVHH INEA*
A.IDMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
NDRQ...IHR ML*

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FIG. 12

1 ccaaaaacaa ctcaaatctc ctccgtcgtc cttactccgc catgggtgac
51 gactccggca tggatgctgt tcagcgacgt ctcatgtttg acgatgaatg
101 cattttggtg gatgagtgtg acaatgtggt gggacatgat accaaataca
151 attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca
201 ttcagcgttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg
251 gtctgcaacc aaggtgacat ttcctttagt atggaccaac acctgttgca
301 gccatccact ctacagagaa tccgagcttg ttcccgaaac gcctgagaga
351 atgctgcaca gaggaxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
401 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
451 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
501 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
551 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
601 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
651 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx tcatgtgcaa aagggtacac
701 tcactgaatg caatttgata tgaaaaccat acacaagctg atatagaaac
751 acaccctcaa ccgaaaagca agcctaataa ttcgggttggt gtcgggtcta
801 ccatcaattg tttttttctt ttaacaactt ttaatctcta tttgagcatg
851 ttgattcttg tcttttctgt gtaagatttt gggtttcgtt tcagttgtaa
901 taatgaacca ttgatgggtt gcaatttcaa gttcctatcg acatgtagtg
951 atctaataaaa

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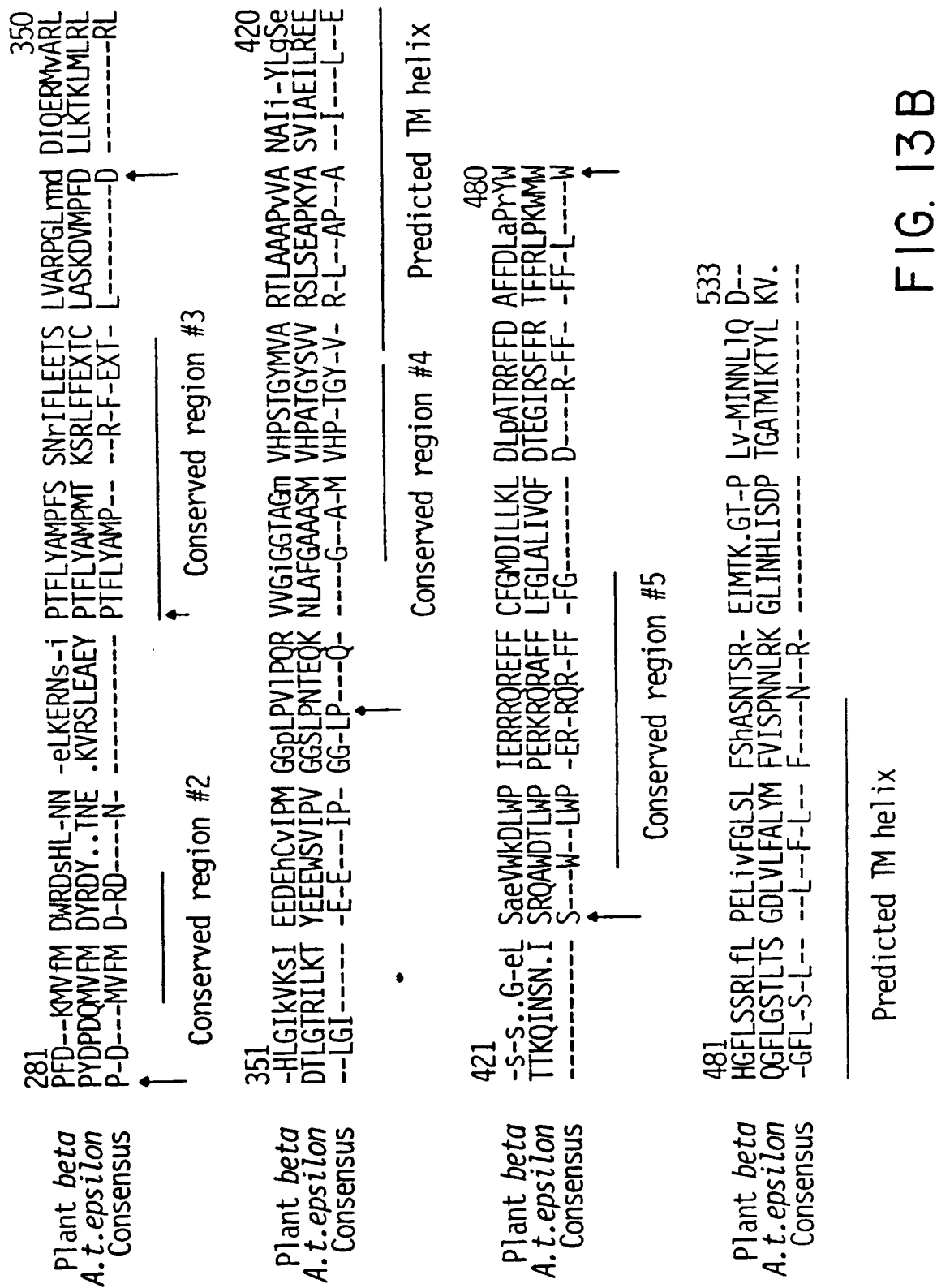


FIG. 13B

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FIG. 14A

Adonis palaestina ε -cyclase cDNA #5

Length: 1898

```

1  aaaggagtgt tctattaatg ttactgtcgc attcttgcaa cacttatatt
51  caaactccat tttcttcttt tctcttcaaa acaacaaact aatgtgagca
101 gagtatctgg ctatggaact acttggtggt cgcaacctca tctcttcttg
151 ccctgtgtgg acttttgga caagaaacct tagtagttca aaactagctt
201 ataacataca tcgatatggt tcttcttgta gagtagattt tcaagtgaga
251 gctgatggtg gaagcgggag tagaagttct gttgcttata aagagggttt
301 tgtggatgaa gaggatttta tcaaagctgg tggttctgag cttttgtttg
351 tccaaatgca gcaaacaaag tctatggaga aacaggccaa gctcgccgat
401 aagttgccac caataccttt tggagaatcc gtgatggact tggttgtaat
451 aggttggtga cctgctggtc tttcactggc tgcagaagct gctaagctag
501 ggttgaaagt tggccttatt ggtcctgac ttccttttac aaataattat
551 ggtgtgtggg aagacgagtt caaagatctt ggacttgaac gttgtatcga
601 gcatgcttgg aaggacacca tcgtatatct tgataatgat gctcctgtcc
651 ttattggtcg tgcatatgga cgagttagtc gacatttgct acatgaggag
701 ttgctgaaaa ggtgtgtgga gtcaggtgta tcatatctgg attctaaagt
751 ggaaaggatc actgaagctg gtgatggcca tagccttgta gtttgtgaaa
801 atgagatctt tatcccttgc aggcttgcta ctgttgcac tggagcagct
851 tcagggaaac ttttgagta tgaagtaggt ggccctcgtg tttgtgtcca
901 aaccgcttat ggggtggagg ttgaggtgga gaacaatcca tacgatccca
951 acttaatggt attcatggac tacagagact atatgcaaca gaaattacag
1001 tgctcggaag aagaatatcc aacatttctC tatgtcatgc ccatgtcgcc
1051 aacaagactt ttttttgagg aaacctgttt ggcccaaaa gatgccatgc
1101 cattcgatct actgaagaga aaactgatgt cacgattgaa gactctgggt
1151 atccaagtta caaaagtta tgaagaggaa tggatcataa ttctgttgg
1201 tggttcttta ccaaacacag agcaaaagaa cctagcattt ggtgctgcag
1251 caagcatggt gcatccagca acaggctatt cggttgtacg gtcactgtca
1301 gaagctccaa aatatgcttc tgtaattgca aagattttga agcaagataa
1351 ctctgcgatg gtggtttctg gacaaagtag tgcagtaaac atttcaatgc
1401 aagcatggag cagtcttttg ccaaaggagc gaaaacgtca aagagcatTc
1451 tttcttttTg gattagagct tattgtgcag ctagatattg aagcaaccag
1501 aacattcttt agaaccttct tccgcttgcc aacttggaatg tgggtggggtt
1551 tccttggttc ttcactatca tctttcgaac tcgtcttggt ttccatgtac
1601 atgtttggtt tggcgccaaa cagcatgagg atgtcacttg tgagacattt
1651 gctttcagat ctttctggtg cagttatggt aagagcttac ctcgaaagggt
1701 agtctcatct attattaaac tctagtgttt caccaaataa atgaggatcc
1751 ttcgaatgtg tatatgatca tctctatgta tatcctgtac tctaattctca
1801 taaagtaaat gccgggtttg atattgttgt gtcaaaccgg ccaatgatat
1851 aaagtaaatt tattgataca aaagtagttt ttttcttaa aaaaaaaa

```


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FIG. 14B

Adonis palaestina ϵ -cyclase #5 predicted polypeptide
TRANSLATE from: 113 to: 1702 Length: 529 amino acids

1	MELLGVRNLI	SSCPVWTFGT	RNLSSSKLAY	NIHRYGSSCR	VDFQVRADGG
51	SGSRSSVAYK	EGFVDEEDFI	KAGGSELLFV	QMQQTKSMEK	QAKLADKLPP
101	IPFGESVMDL	VVIGCGPAGL	SLAAEAACKLG	LKVGLIGPDL	PFTNNYGVWE
151	DEFKDLGLER	CIEHAWKDTI	VYLDNDAPVL	IGRAYGRVSR	HLLHEELLKR
201	CVESGVSYLD	SKVERITEAG	DGHSLVVCEN	EIFIPCRLAT	VASGAASGKL
251	LEYEVGGPRV	CVQTAYGVEV	EVENNPYDPN	LMVFMDYRDY	MOQKLQCSEE
301	EYPTFLYVMP	MSPTRLFFEE	TCLASKDAMP	FDLLKRKLMS	RLKTLGIQVT
351	KVYEEESYI	PVGGSLPNT	QKNLAFGAAA	SMVHPATGYS	VVRSLSEAPK
401	YASVIAKILK	QDNSAYVVSG	QSSAVNISMQ	AWSSLWPKER	KRQRAFFLFG
451	LELIVQLDIE	ATRTEFFRTFF	RLPTWMMWGF	LGSSLSSF DL	VLFSMYMFVL
501	APNSMRMSLV	RHLLSDPSGA	VMVRAYLER*		

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FIG. 15A

DNA sequence of potato cDNA (GenBank R27545) obtained from Nicholas J. Provart

potato.seq Length: 1378 August 2, 1996 13:06 Type: N Check: 605 ..

```

1 tagcggnnnn naggatgagt tcaaagatct tggctttcaa gcctgcattg
51 aacatgtttg gcgggatacc attgtatatc ttgatgatga tgatcctatt
101 cttattggcc gtgcctatgg aagagttagt cgccatttac tgcacgagga
151 gttactcaaa aggtgtgtgg aggcagggtg tttgtatcta aactcgaaag
201 tggataggat tgttgaggcc acaaatggcc acagtcttgt agagtgcgag
251 ggtgatgttg tgattccctg caggtttgtg actgttgcat cgggagcagc
301 ctcggggaaa ttcttgcaat atgagttggg aggtcctaga gtttctgttc
351 aaacagctta tggagtggaa gttgaggtcg ataacaatcc atttgacccg
401 agcctgatgg ttttcatgga ttatagagac tatgtcagac acgacgtca
451 atctttagaa gctaaatata caacatttct ctatgccatg cccatgtctc
501 caacacgagt ctttttcgag gaaacttggt tggcttcaaa agatgcaatg
551 ccattcgatc tgtaaagaa aaaattgatg ttacgattga acaccctcgg
601 tgtaagaatt aaagaaattt atgaggagga atggtcttac ataccagttg
651 gaggatcttt gccaaataca gaacaaaaaa cacttgcaat tgggtgctgct
701 gctagcatgg ttcattccagc cacagggtat tcagtcgtca gatcactgtc
751 tgaagctcca aaatgcgcct tcgtgcttgc aaatatatta cgacaaaatc
801 atagcaagaa tatgcttact agttcaagta ccccgagtat ttcaactcaa
851 gcttggaaca ctctttggcc acaagaacga aaacgacaaa gatcgttttt
901 cctatttgga ctggctctga tattgcagct ggatattgag gggataaggt
951 catttttccg cgcgttcttc cgtgtgccaa aatggatgtg gcagggattt
1001 cttggttcaa gtctttcttn agcagacctc atgttatttg ctttctacat
1051 gtttattatt gcaccaaata acatgagaag aggttaatac agacatcttt
1101 tatctgatcc tactggtgca acattgataa gaacttatct tacattttag
1151 agtaaattcc tcctacaata gttgttgaan nagaggcctc attacttcag
1201 attcataaca gaaatcgagg tctctcgagg ccttgatat aacattttca
1251 ctaggttaat attgcttgaa taagttgcac agtttcagtt tttgtatctg
1301 cttctttttt gtccaagatc atgtattgan ccaatttata tacattgcca
1351 gtatatataa attttataaa aaaaaaaaa

```

poteps.pep Length: 378 TRANSLATE from: 14 to: 1147

```

1 DEFKDLGLQA CIEHVWRDTI VYLDDDDPIL IGRAYGRVSR HLLHEELLKR
51 CVEAGVLYLN SKVDRIEAT NGHSLVECEG DVVIPC RFVT VASGAASGKF
101 LOYELGGPRV SVQTAYGEV EVDNNPFDPS LMVFM DYRDY VRHDAQSLEA
151 KYPTFLYAMP MSPTRVFFEE TCLASKDAMP FDLLKKK LML RLNTLG VRIK
201 EIYEEESYI PYGGSLPNTE QKTAFGAAA SMVHPATGYS VVRSLS EAPK
251 CAFVLANILR QNHSKNMLTS SSTPSISTQA WNTLWPQERK RQRSFF LFLGL
301 ALILQLDIEG IRSFFRAFFR VPKWMWQGFL GSSLSXADLM LFAFYM FIIA
351 PNDMRRGLIR HLLSDPTGAT LIRTYLTF*

```

FIG. 15B

Chimeric lettuce/potato lycopene ϵ -cyclase: converts lycopene to δ -carotene, the lettuce cDNA converts lycopene to ϵ -carotene and the potato cDNA does not produce an active enzyme

(amino acids in lower case are from lettuce and those in uppercase are from the potato cDNA; an *Ava*II site in common to the two cDNAs was used to construct the chimera)

```
1  mecfgarnmt atnavftcpt ftdcnirhkf sllkqrrftn lsassslrqi
51  kcsaksdrcv vdkqgisvac eedyvkaggs elffvqmqrt ksmesqskls
101 eklaqipign cildlvvigc gpaglalaee saklglnvgi igpdlpftnn
151 ygvwqdefig lglegciehs wkdtlvyldd adpirigray grvhrdlhe
201 ellrrcvesg vsylsskver iteapngysl iecegnitip crlatvasga
251 asgkfleyel gGPRVSVQTA YGVEVEVDNN PFDPSLMVFM DYRDYVRHDA
301 QSLEAKYPTF LYAMPMSPTR VFFEETCLAS KDAMPFDLLK KKLMLRLNTL
351 GVRIKEIYEE EWSYIPVGGs LPNTEQKTLA FGAAASMVHP ATGYSVVRSL
401 SEAPKCAFLV ANILRQNHSK NMLTSSSTPS ISTQAWNTLW PQRKRQRFSF
451 FLFGLALILQ LDIEGIRSFF RAFFRVPKWM WQFLGSSLS XADLMLFAFY
501 MFIIAPNDMR RGLIRHLLSD PTGATLIRTY LTF*
```

FIG. 16

GAP comparison of Arabidopsis ϵ -cyclase x potato ϵ -cyclase (partial)
 blosum62.cmp Gap Weight: 12 Average Match: 2.912
 Length Weight: 4 Average Mismatch: -2.003
 Quality: 1485 Length: 529
 Ratio: 3.929 Gaps: 1
 Percent Similarity: 79.893 Percent Identity: 76.139
 Match display thresholds for the alignment(s):
 | = IDENTITY : = 2 . = 1

```

151 EDEFNDLGLQKCIHVWRETIVYLDDDKPITIGRAYGRVSRLLHEELLR 200
    ||| ||||| |||||:||||| ||| ||||| ||||| |||||
1  .DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLK 49

201 RCVESGVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGK 250
    |||.|| ||.|||| | ||..| || |: . ||||| ||||| |||||
50 RCVEAGVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGK 99

251 LLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVMDYRDYTNEKVRSL 300
    |||.||||| ||||| |||||:|. |: ||| ||||| ||||| .|||
100 FLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVEMDYRDYVRHDAQSL 149

301 AEYPTFLYAMPMTKSRLFFETCLASKDVMPFDLLKTKMLRLDTLGIRI 350
    |.||||| |||. .|.||||| ||||| ||||| |||||.|||:|
150 AKYPTFLYAMPMSPTRVFFETCLASKDAMPFDLLKKKMLRLNTLGVRI 199

351 LKTYEEESYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAP 400
    . ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 KEIYEEESYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAP 249

401 KYASVIAEILREETTKQI.....NSNISRQAWDTLWPPERKRQRAFFLFG 445
    || |:| |||: .| . .|| |||.||||| |||||.|||||
250 KCAFVLANILRQNH SKNMLTSSSTPSISTQAWNTLWPQERKRQRSFFLFG 299

446 LALIVQFDTEGIRSFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVI 495
    |||.|| | ||||| |||.||||| |||||. . ||.|||| |:|
300 LALILQLDIEGIRSFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFII 349

496 SPNNLRKGLINHLISDPTGATMIKTYLKV 524
    .||.:|:| |||:||||| |:| |||
350 APNDMRRGLIRHLLSDPTGATLIRTYLTF 378
  
```

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FIG. 17A

Adonis palaestina Ipi1

```
1 attcatcttc agcagcgctg tcgtactctt tctatatctt cttccatcac
51 taacagtagt cgccgacggt tgaatcggct attcgccctca acgtcaacta
101 tgggtgaagt cactgatgct ggaatggatg ctgttcagaa gcggctcatg
151 ttcgacgacg aatgtatctt ggtggatgag aatgacaagg tcgtcgggca
201 tgattccaaa tacaactgtc atttgatgga aaagatagag gcagaaaatt
251 tgcttcacag agccttcagt gttttcttgt tcaactcaaa atatgaattg
301 cttcttcagc aacgatccgc caciaaggta acattcccgc tcgtatggac
351 aaacacatgt tgcagtcac ctctctttcg tgattccgag ctcatagaag
401 aaaattatct cgggtgtacga aacgctgcac aaagaaagct tttagacgag
451 ctaggcattc cagctgaaga tgtcccagtt gatgaattta ctcctcttgg
501 tcgcattctt tacaaagctc catctgacgg caaatgggga gagcacgaat
551 tggactatct cctatcttatt gtccgagatg tgaaatacga tccaaaccca
601 gatgaagttg ctgatgctaa gtatgttaat cgcgaggagt tgagagagat
651 actgagaaaa gctgatgctg gtgaagaggg actcaagttg tctccttggt
701 ttagattggg tggtgataac tttttgttca agtgggtggga tcatgtagag
751 cagggtacga ttaaggaagt tgctgacatg aaaactatcc acaagttgac
801 ttaagaggac ttctctcctc tgttctacta tttgtttttt gctacaataa
851 gtgggtgggtg ataagcagtt tttctgtttt ctttaattta tggcttttga
901 atttgcctcg atgttgaact tgtaacatat ttagacaaat atgagacctt
951 gtaagttgaa tttgaggctg aatttatatt tttgggaaca taataatggt
1001 aa
```

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FIG. 17 B

Adonis palaestina Ipi2

```
1  ttttaaagct ctttcgctcc accaccatca aagccagcca aatttctctg
51  tacaaaagtt aaaaacaccg ctttgggctt tggcccctcc atatcggaat
101 ccttgtttac gatacgcatc taaaccagta attctcgggt ttaatttggt
151 tcctaaatta ggcccctttc cggaatcccc agaattatgt cgtcgatcag
201 gattaatcct ttatatagta tcttctccac caccactaaa acattatcag
251 cttcgtgttc ttctcccgtt gttcatcttc agcagcgttg tcgtactctt
301 tctatttctt cttccatcac taacagtcct cgccgagggt tgaatcggct
351 gttcgcctca acgtcgacta tgggtgaagt cgctgatgct ggtatggatg
401 ccgtccagaa gcggcttatg ttcgacgatg aatgtatttt ggtggatgag
451 aatgacaagg tcgtcggaca tgattccaaa tacaactgtc atttgatgga
501 aaagatagag gcagaaaact tgcttcacag agccttcagt gttttcttat
551 tcaactcaaa atacgagttg cttcttcagc aacgatctgc aacgaaggta
601 acattcccgc tcgtatggac aaacacctgt tgcagccatc ccctcttccg
651 tgattccgaa ctcatagaag aaaattttct cggggtacga aacgctgcac
701 aaaggaagct ttagacgag ctaggcattc cagctgaaga cgtaccagtt
751 gatgaattca ctctcttgg tcgcattctt taaaagctc catctgacgg
801 aaaatgggga gagcacgaac tggactatct tctgtttatt gtccgagatg
851 tgaaatacga tccaaacca gatgaagttg ctgacgctaa gtacgttaat
901 cgcgaggagt tgaaagagat actgagaaaa gctgatgcag gtgaagaggg
951 aataaagttg tctccttggg ttagattggg tgtggataac tttttgttca
1001 agtggtggga tcatgtagag gaggggaaga ttaaggacgt cgccgacatg
1051 aaaactatcc acaagttgac ttaagagaaa gtctcttaag ttctactatt
1101 tgggtttttgc ttcaataagt ggatggtgat gagcagtttt tatgcttcct
1151 ttaatttttg cttttcaatt tgctttatgt gttgaacttg taacatattt
1201 agtcaaatat gagaccttgt gagttgaatt tgaggttata tttatagttt
1251 tggaacata aaaaaaaaaa
```

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FIG. 18A

Haematococcus pluvialis Ipil

```

1   ctcggtagct ggccacaatc gctatttgga acctggcccc gcggcagtcc
51  gatgccgcga tgcttcgttc gttgctcaga ggcctcacgc atatcccccg
101 cgtgaactcc gccagcagc ccagctgtgc acacgcgcga ctccagttta
151 agctcaggag catgcagatg acgctcatgc agcccagcat ctcagccaat
201 ctgtcgcgcg ccgaggaccg cacagaccac atgaggggtg caagcacctg
251 ggcaggcggg cagtcgcagg atgagctgat gctgaaggac gagtgcattc
301 tgggtgatgt tgaggacaac atcacaggcc atgccagcaa gctggagtgt
351 cacaagtcc taccacatca gcctgcaggc ctgctgcacc gggccttctc
401 tgtgttcctg tttgacgatc aggggcgact gctgctgcaa cagcgtgcac
451 gctcaaaaat caccttccca agtgtgtgga cgaacacctg ctgcagccac
501 cctttacatg ggcagacccc agatgaggtg gaccaactaa gccaggtggc
551 cgacggaaca gtacctggcg caaaggctgc tgccatccgc aagtgggagc
601 acgagctggg gataccagcg caccagctgc cggcaagcgc gtttcgcttc
651 ctcacgcgtt tgcactactg tgccgcggac gtgcagccag ctgcgacaca
701 atcagcgctc tggggcgagc acgaaatgga ctacatcttg ttcacccggg
751 ccaacgtcac cttggcgccc aaccctgacg aggtggacga agtcaggtag
801 gtgacgcaag aggagctgcg gcagatgatg cagccggaca acgggctgca
851 atggtcgccg tggtttcgca tcatcgccgc gcgcttcctt gagcgttggt
901 gggctgacct ggacgcggcc ctaaactg acaaacacga ggattgggga
951 acggtgcatc acatcaacga agcgtgaaag cagaagctgc aggatgtgaa
1001 gacacgtcat ggggtggaat tgcgtacttg gcagcttcgt atctcctttt
1051 tctgagactg aacctgcagt caggtccac aaggtcaggt aaaatggctc
1101 gataaaatgt accgtcactt tttgtcgcgt atactgaact ccaagaggtc
1151 aaaaaaaaaa aaaaaa

```

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FIG. 18B

Haematococcus pluvialis Ipi2

```
1  tggaaacctgg cccggcggca gtccgatgcc gcgatgcttc gttcgttgct
51  cagaggcctc acgcatatcc cgcgcgtgaa ctccgcccag cagcccagct
101 gtgcacacgc gcgactccag ttttaagctca ggagcatgca gctgcttgcc
151 gaggaccgca cagaccacat gaggggtgca agcacctggg caggcgggca
201 gtcgcaggat gagctgatgc tgaaggacga gtgcatctta gtggatgctg
251 acgacaacat cacaggccat gccagcaagc tggagtgcc acaattccta
301 ccacatcagc ctgcaggcct gctgcaccgg gccttctctg tgttcctgtt
351 tgacgaccag gggcgactgc tgctgcaaca gcgtgcacgc tcaaaaatca
401 ccttcccaag tgtgtggacg aacacctgct gcagccaccc tctacatggg
451 cagaccccag atgaggtgga ccaactaagc caggtggccg acggcacagt
501 acctggcgca aaagctgctg ccatccgcaa gttggagcac gagctgggga
551 taccagcgca ccagctgccg gcaagcgcgt ttcgcttcct cagcgtttg
601 cactactgtg ccgcggacgt gcagccggct gcgacacaat cagcgtctg
651 gggcgagcac gagatggact acatcttatt catccggggc aacgtcacct
701 tggcgcccaa ccctgacgag gtggacgaag tcaggtacgt gacgcaagag
751 gagctgcggc agatgatgca gccggacaac gggttgcaat ggtcgccgtg
801 gtttcgcac ctcgccgcgc gcttccttga gcgttggtgg gctgacctgg
851 acgcggccct aaacactgac aaacacgagg attggggaac ggtgcatcac
901 atcaacgaag cgtgaaggca gaagctgcag gatgtgaaga cacgtcatgg
951 ggtggaattg cgtacttggc agcttcgtat ctctttttc tgagactgaa
1001 cctgcagagc tagagtcaat ggtgcatcat attcatcgtc tctcttttgt
1051 tttagactaa tctgtagcta ggtcactga tgaatccttt acaactttca
1101 aaaaaaaaa
```


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FIG. 19A

Lactuca sativa Ipi1

1	tgccaaaatg	ttgaaatttc	ccccttttaa	aaccattgct	accatgatct
51	cttctccata	ttcttccttc	ttgctgcctc	ggaaatcttc	tttccctcca
101	atgccgtctc	tcgcagccgc	tagtgttttc	ctccaccctc	tttcgtctgc
151	cgctatgggc	gattccagca	tggatgctgt	ccagcgacgt	ctcatgttcg
201	atgacgaatg	cattttgggtg	gatgagaatg	acaaagtggg	tggccatgat
251	actaaataca	attgtcattt	gatggagaag	attgaaaagg	gaaatatgct
301	acacagagca	ttcagtgtgt	tcttgttcaa	ctcgaaatat	gaattactcc
351	ttcagcaacg	ttctgcaacc	aaggtagactt	tccctttggg	atggacaaaac
401	acgtgttgca	gccatccact	atacagggag	agtgagctta	ttgacgaaaa
451	cgcccttggg	gtgaggaatg	ctgcacagag	gaagctcctg	gatgaactcg
501	gcatccctgg	agcagatgtt	ccggttgatg	agttcactcc	attgggtcgc
551	attctataca	aggccgcctc	ggatggaaaag	tggggagaaac	atgaacttga
601	ttacctgctg	tttatgggtac	gtgatgttgg	tttggatccg	aaccacagatg
651	aagtgaaga	tgtaaaatat	gtgaaccggg	aagagctgaa	ggaattggta
701	aggaaggcgg	atgctgggtga	agaggggtgtg	aagctgtccc	cgtggttcaa
751	attgattgtc	gataatttct	tgtttcagtg	gtgggatcga	ctccataagg
801	gaaccctaac	cgaagctatt	gatatgaaaa	caatccacaa	actcacataa
851	aaacactaca	ctagtaggag	agaggattat	atgagatatt	tggtatatgt
901	gaaattgaaa	ttcagatgaa	tgcttgtatt	tatttctatt	tggacaaact
951	tcaacttctt	tttgctacct	tatcagaaaa	aaaaa	

FIG. 19B

Lactuca sativa Ipi2

1	tattcgcttc	aaaatctctt	ccattaactg	ctcaaattctc	caccttcgcc
51	ggtcttaatc	tccgccggcg	cactttcacc	accataaccg	ccgccatggg
101	tgacgattcc	ggcatggacg	ctgtccagag	acgtctcatg	tttgatgatg
151	aatgcatttt	ggttgatgaa	aatgacaatg	ttcttgggca	tgataccaaa
201	tacaattgtc	acttgatgga	gaagattgag	aaagataatt	tgcttcatag
251	agcattcagt	gtatttttat	tcaattcaaa	atacgaatta	ctccttcagc
301	aaaggtcaga	aaccaagggtg	acatttcctt	tggtatggac	aaacacctgt
351	tgcagccatc	cactatacag	agaatcggag	ttaattcccg	aaaatgccct
401	tggggtcaga	aatgctgcac	agaggaagct	tctagatgaa	ctcggatatcc
451	ctgctgaaga	tgttccagtt	gatgagttca	caacttttagg	tcgcatgttg
501	tacaaggctc	catctgatgg	aaaatggggg	gaacatgaag	ttgattacct
551	actcttcctc	gtgctgacg	ttgccgtgaa	cccaaaccct	gatgaggtgg
601	cggacattag	atacgtgaac	caagaagagt	taaaagagtt	actaaggaag
651	gcggatgcgg	gtgaggaggg	tttgaaattg	tccccatggt	ttaggctagt
701	ggtggacaac	ttcttgttca	aatggtggga	tcatgtccaa	aaggggacac
751	tcaatgaagc	aattgacatg	aaaaccattc	ataagttgat	atgaaaaatg
801	gttaatatft	atggtgggtg	tttgagacta	ataatttgtg	tggtcaagtc
851	tcggtccttc	tttttttaac	gttttttttt	tttcttttat	tgggagtggt
901	tattgtgtac	ttgtaacgta	ggccctttgg	ttacgcttta	agagtttaat
951	aaagaaccac	cgtaatttta	aaaaaaaaaa	aaaaaaaa	

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FIG. 20

Chlamydomonas reinhardtii Ipil

(Note: the isomerase cDNA probably ends at ca. base 1103; the second half of the cDNA is similar to extensin and other hydroxyproline-rich structural proteins)

```

1  ggcacgagct cgagtttggt ttaccatgac atcgggaatt tggaagcttg
51  aactacctca attactcaag taactcgcg caacacattt cgcgcgcca
101 cgctgttttc tctgtccag ctaccgagca gcattgcttt agatcgcttt
151 gatgtcataa actcccactt atatgagatc cagtttcacg gagcccaagc
201 ccagagcgca acctgtctta agccgcggca gggcgcccat gcgcctcgcg
251 caaagccgtg ctctcgttgc gcggtgcagc tccgccctgt ggccgggagc
301 aggactttca caggctcaaa gcggtgcggt gcgaatggcg agttcgtcaa
351 cctgggaagg cacgggcctg agccaggatg acttcatgca gcgggacgag
401 tgcttggtgg tggacgagca ggaccggctg ctaggcaccg ccaacaagta
451 cgactgccac cgcttcgagg cggccaaggg ccagccctgc ggccgcctgc
501 accgcgcctt ctccgtgttc ctgttcagcc ccgacggccg actgctgctg
551 cagcagcgcg cagccagcaa ggtgacgttc ccgggtgtgt ggaccaacac
601 ctgctgctcg caccgctgg cgggccaggc gccggacgag gtggacctgc
651 cggcggcggt agcctcgggc caggtgccgg gcatcaaggc ggcggcggtg
701 cgcaagctgc agcacgagct ggggataccg ccggagcagg ttcccgcctc
751 ctccctctcc ttcctcacgc gtctgcacta ctgcgccgcc gacaccgcca
801 cgcacggccc ggcggcggag tggggcgagc acgaggtgga ctacgtgctg
851 ttcgtgcggc cgcagcagcc cgtcagcctg cagcccaacc cagacgaggt
901 ggacgccacg cgctacgtga cgctgccgga gcttcagtcc atgatggcgg
951 accccggcct cagctggagc ccctggttcc gcatcctggc cacacagccc
1001 gccttcctgc ccgcctggtg gggcgacctg aagcggcgct ggcccccggg
1051 cggcagccga ctgtaggact ggggcaccat ccaccgcgtc atgtgaagaa
1101 aaaggggaag caggggcggg agcgggggat gaatgggaat gtgaatgcga
1151 ttgtgatgcg gcgtgggatg aggtctgaag acagggggaa aatcgggggg
1201 cgggcgtgag cgtgtgtgta cgtgagcgac aaagccggga ggcggaccgc
1251 gcgatgggta catgtgtgtg cggagggtcg gtgggtcggg cggttgcgcg
1301 gcatagcgtg ttgtgtgtgt gcggctgcgc gggatatgtg gcacccgggc
1351 acggaggaga aggcacacgc aggtggcgcg gaggtgtgtc aggggccatg
1401 ggccggcctc actcctggtc gtgccagtg gtctcgtggg cagagtggca
1451 ggggctgcac ccatatgagc ggcgcactgc cgcgctgggc taagtcctta
1501 tcacttggtg aggtggggcg aggtggctgt gggcggcggg cgcagtggca
1551 gaaggacacg gtgtgtgagc ggtggagctc tggccgtgcc ggccgtgagg
1601 ggcggatagc gatatgacgt tgtgcttggc cgctgtaatg cgggagaatg
1651 tgcaggccgc gagaagcggg cggtggcagg aggccgcagg ctgcagcacc
1701 cgttggggag gtgccgcctg caggcgcgcc gccgggcggg cctgagtaat
1751 gggcgccctg gtagtggcgg ccacaggagg cgcaggaggc agcagcagga
1801 ggacgagctg gagggacccg ttggcaaccc aaggttgcg cgtgtaacata
1851 gtggccatac aaaaaaaaaa aaaa

```

FIG. 21A

Tagetes erecta Ipil

1	ccaaaaacaa	ctcaaattctc	ctccgtcgc	cttactccgc	catgggtgac
51	gactccggca	tggatgctgt	tcagcgacgt	ctcatgtttg	acgatgaatg
101	catttttggtg	gatgagtgtg	acaatgtggt	gggacatgat	accaaataca
151	attgtcactt	gatggagaag	attgaaacag	gtaaaatgct	gcacagagca
201	ttcagcgttt	ttctattcaa	ttcaaaatac	gagttacttc	ttcagcaacg
251	gtctgcaacc	aaggtgacat	ttcctttagt	atggaccaac	acctgttgca
301	gccatccact	ctacagagaa	tccgagcttg	ttcccgaaaa	cgcccttgga
351	gtaagaaatg	ctgcacagag	gaagctgttg	gatgaactcg	gtatccctgc
401	tgaagatggt	cccgttgatc	agtttactcc	tttaggtcgc	atgctctaca
451	aggctccatc	tgatggaaa	tggggagaac	atgaacttga	ctacctactt
501	ttcatagtga	gagacgttgc	tgtaaacccg	aaccagatg	aagtggcgga
551	tatcaaatat	gtganccang	aagagttaaa	ggagctgcta	aggaaagcag
601	atgcggggga	ggagggtttg	aagctgtctc	catggttcag	gttagtggtt
651	gataacttct	tgttcaagt	gtgggatcat	gtgcaaaagg	gtacactcac
701	tgaagcaatt	gatatgaaaa	ccatacacaa	gctgatatag	aaacacaccc
751	tcaaccgaaa	agttcaagcc	taataattcg	ggttgggtcg	ggtctaccat
801	caattgtttt	tttcttttaa	gaagttttaa	tctctatttg	agcatgttga
851	ttcttgtctt	ttgtgtgtaa	gattttgggt	ttcgtttcag	ttgtaataat
901	gaaccattga	tggtttgcaa	tttcaagttc	ctatcgacat	gtagtgatct
951	aaaaaa				

FIG. 21B

Oryza sativa Ipil

1	cctccctttg	cctcgcgcag	aggcggccgc	gccttctccg	ccgcgaggat
51	ggccggcgcc	gccgccgcg	tggaggacgc	cgggatggac	gagggtccaga
101	agcggctcat	gttcgacgac	gaatgcattt	tgggtggatga	acaagacaat
151	gttgttggcc	atgaatcaaa	atataactgc	catctgatgg	aaaaaatcga
201	atctgaaaat	ctacttcata	gggctttcag	tgtattcctg	ttcaactcaa
251	aatatgaact	cctactccag	caacgatctg	caacaaagg	tacatttcct
301	ctagtttgga	ccaacacttg	ctgcagccat	cctctgtacc	gtgagtctga
351	gcttatacag	gaaaactacc	ttgggtgttag	aaatgctgct	cagaggaagc
401	tcttggaatga	gctgggcatc	ccagctgaag	atgtgccagt	tgaccaattc
451	acccctcttg	gtcggatgct	ttacaaggcc	ccatctgatg	gaaaatgggg
501	tgaacacgag	cttgactacc	tgctgttcat	cgtccgcgac	gtgaaggtag
551	tcccgaaccc	ggacgaagt	gccgatgtga	aatacgtgag	ccgtgagcag
601	ctgaaggagc	tcatccgcaa	agcggacgcc	ggagaggaag	gcctgaagct
651	gtctccctgg	ttccggctgg	ttgttgacaa	cttctctatg	ggctggtggg
701	atcacgtcga	gaaaggcacc	ctcaacgagg	ccgtggacat	ggagaccatc
751	cacaagctga	agtaaggact	gcgatgttgt	ggctggaaag	aatgatcctg
801	aagactctgt	tcttgtgctg	ctgcatatta	ctcttaccag	ggaagtgtga
851	gaagtcagaa	gaagcttttg	tatgtttctg	ggtttggagc	ttggaagtgt
901	tgggctctgc	tgactgagag	attcccttat	agagtgtcta	tgtaatttta
951	gcaaacttct	atattataca	tgattagtta	attgttcggt	gtctgaataa
1001	agaacaatag	catgttccat	gtttatttgc	t	

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ClustalW 1.7 Multiple Sequence Alignment of Plant and Green Algal Isopentenyl Pyrophosphate Isomerases (IPI)
These amino acid sequences were predicted by cDNAs that were isolated and identified by color complementation in *E.coli*

1	15	16	30	31	45	46	60	61	75	76	90
1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	27
2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	75
3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	27
4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	90
5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	29
6	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	33
7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	80
8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	29
9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	74
10	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	86
11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	84
1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	107
2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	155
3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	107
4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	170
5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	109
6	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	113
7	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	160
8	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	109
9	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	162
10	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	174
11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	174

FIG. 22A

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	181	195	196	210	211	225	226	240	241	255	256	270
1 <i>T. erecta</i> 1	AQRKLLDELGIPAED	VPVDQFTPLGRMLY-	--KAPSDG----	KWG	EHELDYLLFIVRD--	VAVNPNPDEVADIKY	VSHEELKELLRKADA	188				
2 <i>L. sativa</i> 1	AQRKLLDELGIPGAD	VPVDEFTPLGRILY-	--KAASDG----	KWG	EHELDYLLFIVRD--	VGLDPNPDEVKOVKY	VNREELKELVRKADA	236				
3 <i>L. sativa</i> 2	AQRKLLDELGIPAED	VPVDEFTPLGRMLY-	--KAPSDG----	KWG	EHEVDYLLFIVRD--	VAVNPNPDEVADIRY	VNQEELKELLRKADA	188				
4 <i>A. palaestina</i> 2	AQRKLLDELGIPAED	VPVDEFTPLGRILY-	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKYDPNPDEVADAKY	VNREELKEILRKADA	251				
5 <i>A. palaestina</i> 1	AQRKLLDELGIPAED	VPVDEFTPLGRILY-	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKYDPNPDEVADAKY	VNREELREILRKADA	190				
6 <i>O. sativa</i> 1	AQRKLLDELGIPAED	VPVDQFTPLGRMLY-	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKVVPNPDEVADVKY	VSREQLKELIRKADA	194				
7 <i>A. thaliana</i> 1	AQRKLLDELGIVAED	VPVDEFTPLGRMLY-	--KAPSDG----	KWG	EHELDYLLFIVRD--	VKVQPNPDEVAEIKY	VSREELKELVKKADA	241				
8 <i>A. thaliana</i> 2	AQRKLFDELGIVAED	VPVDEFTPLGRMLY-	--KAPSDG----	KWG	EHEVDYLLFIVRD--	VKLQPNPDEVAEIKY	VSREELKELVKKADA	190				
9 <i>H. pluvialis</i> 1	AIRKLEHELGIPIAHQ	LPASAFRELTRLHYC	AADVQPAATQSALWG	EHEMDYILFIRAN--	VTLPAPNPDEDEVRY	VTQEELRQWQP----	247					
10 <i>H. pluvialis</i> 2	AIRKLEHELGIPIAHQ	LPASAFRELTRLHYC	AADVQPAATQSALWG	EHEMDYILFIRAN--	VTLPAPNPDEDEVRY	VTQEELRQWQP----	259					
11 <i>C. reinhardtii</i> 1	AVRKLQHELGIPIPEQ	VPASSFSFLTRLHYC	AADTATHG--PAAEWG	EHEVDVWLFVRRQPQ	VSLQPNPDEVADTRY	VTLPQLQSWMA----	259					
	271	285	286	300	301	315	316					
1 <i>T. erecta</i> 1	GEEGLKSPWFLRV	DN--FLFKMWDHVQK	GTL----	TEAIDMKTI	HKLI--	232	<i>Tagetes erecta (marigold)</i>					
2 <i>L. sativa</i> 1	GEEGVKSPWFKLIV	DN--FLFKMWDRLHK	GTL----	TEAIDMKTI	HKLI--	280	<i>Lactuca sativa (romaine lettuce)</i>					
3 <i>L. sativa</i> 2	GEEGLKSPWFLRV	DN--FLFKMWDHVQK	GTL----	NEAIDMKTI	H-----	229	<i>Lactuca sativa (romaine lettuce)</i>					
4 <i>A. palaestina</i> 2	GEEGKLSWFLRV	DN--FLFKMWDHVEE	GKI----	KDVADMKTII	HKLI--	295	<i>Adonis palaestina (pheasant's eye)</i>					
5 <i>A. palaestina</i> 1	GEEGLKSPWFLRV	DN--FLFKMWDHVEQ	GTL----	KEVADMKTII	HKLI--	234	<i>Adonis palaestina (pheasant's eye)</i>					
6 <i>O. sativa</i> 1	GEEGLKSPWFLRV	DN--FLMGMDHVEK	GTL----	NEAVDMETI	HKLK--	238	<i>Oryza sativa (rice)</i>					
7 <i>A. thaliana</i> 1	GEEGLKSPWFLRV	DN--FLMKMWDHVEK	GTL----	VEAIDMKTI	HKL---	284	<i>Arabidopsis thaliana</i>					
8 <i>A. thaliana</i> 2	GDEAVKLSWFLRV	DN--FLMKMWDHVEK	GTL----	TEAADMKTII	HKL---	233	<i>Arabidopsis thaliana</i>					
9 <i>H. pluvialis</i> 1	-DNGLQSWPFRIIA	AR--FLERWADLDA	ALN--	TDKHEDWGTIV	HHINEA	293	<i>Haematococcus pluvialis</i>					
10 <i>H. pluvialis</i> 2	-DNGLQSWPFRIIA	AR--FLERWADLDA	ALN--	TDKHEDWGTIV	HHINEA	305	<i>Haematococcus pluvialis</i>					
11 <i>C. reinhardtii</i> 1	-DPGLSWSPWFRILA	TOPAFLPAMWGDLKR	RWRPGGSRLSDWGTII	HRVM--	307	<i>Chlamydomonas reinhardtii</i>						

FIG. 22B

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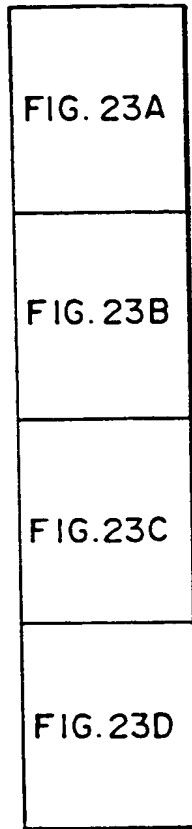


FIG. 23

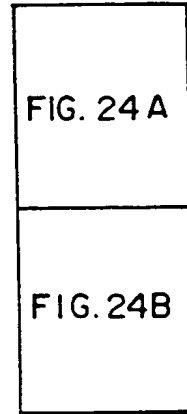


FIG. 24

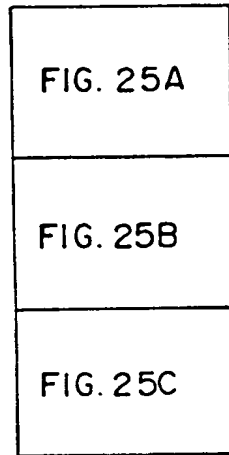


FIG. 25

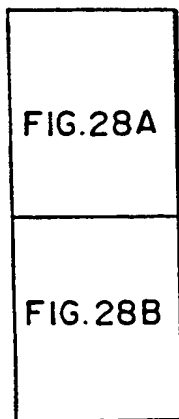


FIG. 28

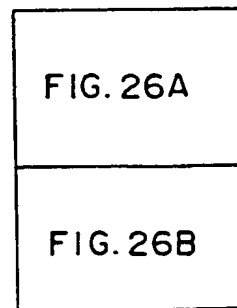


FIG. 26

FIG. 23A

Comparison using GAP program of the Genetics Computer Group
 Gap Weight: 50 Average match: 10.000
 Length Weight: 3 Average Mismatch: 0.000
 Quality: 17392 Length: 1904
 Ratio: 9.411 Gaps: 3
 Percent Similarity: 95.331 Percent Identity: 95.331
 Match display thresholds for the alignment(s):
 | = IDENTITY : = 5 . = 1

Adonis palaestina ε -cyclase #3 x *Adonis palaestina* ε -cyclase #5

```

1 gagagaaaaagagtgttatattaatgttactgtcgcattcttgcaacac. 49
      |||||
1 .....aaaggagtgttctattaatgttactgtcgcattcttgcaacact 44
      |||||
50 .atattcagactccatcttctgtttctcttcaaaacaacaaactaatg 98
      |||||
45 tatattcaaactccatcttctcttcttcttcaaaacaacaaactaatg 94
      |||||
99 tga.cggagtatctagctatggaactacttgggtgttcgcaacctcatctc 147
      |||||
95 tgagcagagtatctggctatggaactacttgggtgttcgcaacctcatctc 144
      |||||
148 ttcttgccctgtctggacttttggaacaagaaaccttagtagttcaaaac 197
      |||||
145 ttcttgccctgtgtggacttttggaacaagaaaccttagtagttcaaaac 194
      |||||
198 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 247
      |||||
195 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 244
      |||||
248 gtgagggctgatggtggaagcgggagtagaacttctgttgcttataaaga 297
      |||||
245 gtgagagctgatggtggaagcgggagtagaagttctgttgcttataaaga 294
      |||||
298 gggttttgtggacgaggaggattttatcaaagctggtggttctgagctti 347
      |||||
295 gggttttgtggatgaagaggattttatcaaagctggtggttctgagcttt 344
      |||||
348 tgtttgtccaaatgcagcaaacaagtctatggagaaacaggccaagctc 397
      |||||
345 tgtttgtccaaatgcagcaaacaagtctatggagaaacaggccaagctc 394
      |||||

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FIG. 23C

948 atcccaacttaatggtatttattggactacagagactatatgcaacagaaa 997
|||||
945 atcccaacttaatggtattcatggactacagagactatatgcaacagaaa 994
|||||
998 ttacagtgctcggagaagaatatccaacatttctctatgtcatgcccatt 1047
|||||
995 ttacagtgctcggagaagaatatccaacatttctctatgtcatgcccatt 1044
|||||
1048 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1097
|||||
1045 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1094
|||||
1098 ccatgccttctgatctactgaagagaaaaactaatgtcacgattgaagact 1147
|||||
1095 ccatgccattctgatctactgaagagaaaaactgatgtcacgattgaagact 1144
|||||
1148 ctgggtatccaagttacaaaatttatgaagaggaatggcttattattcc 1197
|||||
1145 ctgggtatccaagttacaaaagtttatgaagaggaatggctatatattcc 1194
|||||
1198 tggtgggggttctttaccaaacacagagcaaaagaacctagcatttggtg 1247
|||||
1195 tggtggtggttctttaccaaacacagagcaaaagaacctagcatttggtg 1244
|||||
1248 ctgcagcaagcatggtgcatccagcaacaggctattcgggtgtacgatca 1297
|||||
1245 ctgcagcaagcatggtgcatccagcaacaggctattcgggtgtacgggtca 1294
|||||
1298 ctatcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1347
|||||
1295 ctgtcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1344
|||||
1348 agataactctgcatatgtggtttctggacaaagcagtgcagtaaacattt 1397
|||||
1345 agataactctgcatatgtggtttctggacaaagtagtgcagtaaacattt 1394
|||||
1398 caatgcaagcatggagcagcttttggccaaaggagcgaaaacgtcaaaga 1447
|||||
1395 caatgcaagcatggagcagcttttggccaaaggagcgaaaacgtcaaaga 1444
|||||
1448 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1497
|||||
1445 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1494
|||||

1498 aaccagaacggtcctttagaaccttcttccgcttgccaacttggaatgtggt 1547
1495 aaccagaacattcctttagaaccttcttccgcttgccaacttggaatgtggt 1544
1548 ggggtttccttggtccttcaactatcatcttccgatcttgattgttttcc 1597
1545 ggggtttccttggtccttcaactatcatcttccgatctcgctcttgattgttttcc 1594
1598 atgtacatgtttgttttggccccgaacagcatgaggatgtcacttgtgag 1647
1595 atgtacatgtttgttttggcgccaaacagcatgaggatgtcacttgtgag 1644
1648 acatttgctttcagatccttctggtgcagttatggttaaagcttacctcg 1697
1645 acatttgctttcagatccttctggtgcagttatggttaaagagcttacctcg 1694
1698 aaaggtaatc...tgttttatgaaactatagtgtctcattaaataaatga 1744
1695 aaaggtagtctcatctattattaaactctagtgtttcaccaaataaatga 1744
1745 ggatccttcgtatatgtatatgatcatctctatgtatatcctatatattcta 1794
1745 ggatccttcgaatgtgtatatgatcatctctatgtatatcctgtactcta 1794
1795 atctcataaagtaatcgaaaattcattgataaaaaaaaaaaaaaaaaaaaa 1844
1795 atctcataaagtaaatgccgggttgataattgttgtgtcaaaccggccaa 1844
1845 aaaa..... 1848
1845 tgatataaagtaaatatttattgatacaaaagtagtttttttttttaaaaaa 1894

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FIG. 24A

GAP program of Genetics Computer Group
blosum62.cmp

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	2728	Length:	530
Ratio:	5,147	Gaps:	0
Percent Similarity:	99,623	Percent Identity:	99.057

Match display thresholds for the alignment(s):
| = IDENTITY : = 2 . = 1

Adonis palaestina ε -cyclase #3 x *Adonis palaestina* ε -cyclase #5

```

1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50
  ||||||||||||||||||||||||||||||||||||||||||||||||
1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50

51 SGSRTSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100
  |||.||||||||||||||||||||||||||||||||||||||||||
51 SGSRSSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100

101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPTNNGVWE 150
  ||||||||||||||||||||||||||||||||||||||||||||
101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPTNNGVWE 150

151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200
  ||||||||||||||||||||||||||||||||||||||||||||
151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200

201 CVESGVSYLNSKVERITEAGDGHSLVVCENDIFIPCLATVASGAASGKL 250
  |||||.|||||||||||||||||||:||||||||||||||
201 CVESGVSYLDSKVERITEAGDGHSLVVCENEIFIPCLATVASGAASGKL 250

251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300
  ||||||||||||||||||||||||||||||||||||||||||||
251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300

301 EYPTFLYVMPMSPTRLFEEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350
  ||||||||||||||||||||||||||||||||||||||||||||
301 EYPTFLYVMPMSPTRLFEEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350

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351 KIYEEWSYIPVGGSLPNT[•]EQKNLAFGAA[•]SMVHPATGY[•]SVVRSLS[•]EAPK 400
|:|||||||||||||||||||||||||||||||||||||||||
351 KVYEEWSYIPVGGSLPNT[•]EQKNLAFGAA[•]SMVHPATGY[•]SVVRSLS[•]EAPK 400

401 YASVIAKILKQDNSAYVVSGQSSAVNISM[•]QAWSSLWPKERKRQRAFFLFG 450
|||||||||||||||||||||||||||||||||||||||||
401 YASVIAKILKQDNSAYVVSGQSSAVNISM[•]QAWSSLWPKERKRQRAFFLFG 450

451 LELIVQLDIEATRTFFRTFFRLPTW[•]MMWGFLGSSLSSFDLVLF[•]SMYMFVL 500
|||||||||||||||||||||||||||||||||||||||||
451 LELIVQLDIEATRTFFRTFFRLPTW[•]MMWGFLGSSLSSFDLVLF[•]SMYMFVL 500

501 APNSMRMSLV[•]RHLLSDPSGAV[•]MVKAYLER* 530
|||||||||||||||||||||:|||||
501 APNSMRMSLV[•]RHLLSDPSGAV[•]MVRAYLER* 530

FIG. 24B

FIG. 25A

PotatoF :
 ArabidopsisE : MECVGARNF--AAMAVSTFPSWS--CRRKFPVVKRYSYRNIRFGL--CSV--RASGGSSGSESCVAREDF--ADEEDFVKAGSEILFVQVQKQKMDQESKLVDPIS : 103
 AdonisE1 : MELLGVRNL-----ISSCPVMT--FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGRSVAVKEGF--VDEEDFKAGSELLFVQVQKTKSMEKQAKLADKLPPI : 102
 AdonisE2 : MELLGVRNL-----ISSCPVMT--FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGRSVAVKEGF--VDEEDFKAGSELLFVQVQKTKSMEKQAKLADKLPPI : 102
 LettuceEE : MECFGARWMTATMAVFTCPRTDCNIRHKFSLLKQRFNLISA--SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVYKAGSELFFVQVQRTKSMESQSKLSEKJAQIP : 107
 TomatoE : MECVGQNV--GAMAVLTPRLN-----RMSGGELCQEKIFLAY-EQY--ESKCNSSSGSDSCVVDKEDF--ADEEDYKAGSQVLFVQVQKQKMDQESKLSDEL : 100
 MarigoldE : MSMRAG--HMTATMAAFTCPRM-----TSIRYT-----KQIKCNAKQSQ--LVVQKEI--EEEEYVYKAGSELLFVQVQKQKMDQESKLSDEL : 84
 ArabidopsisB : -----MDTLTKTPNKLDFFIPQHGFE--RLCSNPHYHSRVRGKVKRAIKIV-----SSVVGSAALLDLVPETKKNLDFEL : 72
 AdonisB : -----MDTLRTHNKLELLPTLHGFA--EKQHLVSTSKLQNVFRIASRNTH--PCRNQTVKARGSALLELVPETKKNLEFDL : 75
 PepperB : -----MDTLRTPNNLEFL--HGFG--VKVSASFSSVKQKFGAKKFCCEGLG--SRSCVCKASSALLELVPETKKNLEFDL : 71
 TomatoB : -----MDTLTKTPNNLEFLNPHGF--AVKASTFRSEKHNFHFGSRKFCETL--GRSVCVKGSSALLELVPETKKNLEFDL : 73
 TobaccobB : -----MDTLTKTPNKLEFLHPVHGF--VKASSFNSVKPHKFGSRKICENMG--KGVCVKAKSSALLELVPETKKNLEFDL : 73
 MarigoldB : -----MDTLRTYNSFEFVHPSNKFAGNLNQLNQSKSQFQDFRGPCKSQKLGQKYCVKASSALLELVPEIKKNLEFDL : 80
 DaffodiB : -----MDTLRTHNRLELLYPLHELA--KRHFLSPSPNPQNPNFKFSRKPQYQKCRNGYIGVSSNQLLDLVPETKKNLEFDL : 77

PotatoF :
 ArabidopsisE : IG-----DGAIDHWVIGCGPAGLAAESAKLGLKVGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVEA : 54
 AdonisE1 : FG-----ESWMDLVVIGCGPAGLSLAAEAAKGLKVGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 205
 AdonisE2 : FG-----ESWMDLVVIGCGPAGLSLAAEAAKGLKVGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 204
 LettuceEE : IG-----NCTILDLVWIGCGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWQDEFFIGLGECCIEHAWKOTIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 204
 TomatoE : AG-----QTVLDLVVIGCGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 209
 MarigoldE : IGGGDSNCTILDVWIGCGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 202
 ArabidopsisB : PLYDTSKQVVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 191
 AdonisB : PAYDPSRGTVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 181
 PepperB : PMYDPSKGVVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 184
 TomatoB : PMYDPSKGVVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 180
 TobaccobB : PMYDPSKGLVVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 182
 MarigoldB : PMYDPSRNVVDLAVVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 182
 DaffodiB : PLYDPSKALTLVWVGGPAGLAAESAKLGLNVLGILGPDIP-----FTNNYGVWDEFFNDLGLQKQIEHAWRETIVYLDODDPIILIGRAYGRVSRHLHEELLKRCVES : 189

PotatoE : GVLVLSKVDRIVEATNGHSLVECEGDVITPCRFVTVASGAAGKFLQVLEGGPRVSVQTAYGVEVEVDNHPFDPSPUMVFMVYRDY : 240 * 260 * 280 * 300 * 320 *
 ArabidopsisE : GVSYLSSKVDITEASDGLRLVACDDNMVTPCRLATVASGAAGKLLQVEVGPRVCVQTAYGVEVEVENSYPDPQVVFMDYRDY : 161
 AdonisE1 : GVSYLDSKVERITEAGDGHSLVVCENEIFPCRLATVASGAAGKLLQVEVGPRVCVQTAYGVEVEVENSYPDPQVVFMDYRDY : 312
 AdonisE2 : GVSYLNSKVERITEAGDGHSLVVCENEIFPCRLATVASGAAGKLLQVEVGPRVCVQTAYGVEVEVENSYPDPQVVFMDYRDY : 311
 LettuceEE : GVSYLSSKVERITEAPNGYSLICEGNTIPCRFVTVASGAAGKFLQVLEGGPRVCVQTAYGVEVEVENSYPDPQVVFMDYRDY : 311
 TomatoE : GVLVLSKVDRIVEATNGHSLVECEGDVITPCRFVTVASGAAGKFLQVLEGGPRVCVQTAYGVEVEVDNHPFDPSPUMVFMVYRDY : 316
 MarigoldE : GVSYLSSKVERITEAPNGLSLICEGNTIPCRFVTVASGAAGKLLQVLEGGPRVCVQTAYGVEVEVDNHPFDPSPUMVFMVYRDY : 309
 ArabidopsisB : GVKFHQSKVTNVH-EEANSVTVCSGVKIQASWLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 298
 AdonisB : GVKFHQAKVIVH-EESKSLICNDGITINATVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 288
 PepperB : GVKFHQAKVIVH-EESKSLICNDGITINATVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 291
 TomatoB : GVKFHQAKVIVH-EESKSLICNDGITINATVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 287
 TobaccoB : GVKFHQAKVIVH-EESKSLICNDGITINATVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 289
 MarigoldB : GVKFHQAKVIVH-EELKSLICNDGITINATVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 289
 DaffodilB : GVRFHQAIVVKAMH-EEEKSYLICS DGVTIDARVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 296
 : GVRFHQAIVVKAMH-EEEKSYLICS DGVTIDARVLDATG-FSRCLVQYD-KPYNPGVQVAYGIMAEVEEHPEFDLQVLFMDVDRSHLNEKLELKOKNRK : 292

PotatoE : SPTRVFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 340 * 360 * 380 * 400 * 420 * 440
 ArabidopsisE : TKSRLFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 271
 AdonisE1 : SPTRLFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 420
 AdonisE2 : SPTRLFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 421
 LettuceEE : SPTRVFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 421
 TomatoE : SPTRVFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 426
 MarigoldE : SPTRVFFETCJASKDAMPFDLLKKKLMRLNTEIGVRIKETIYEELWSYIPVGGSLPNTTEQKTLAFGAASVWHPATGYSVVRSLSEAPKCAFVLANTLRQNHSKNMLTSS : 418
 ArabidopsisB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 408
 AdonisB : SSKIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 393
 PepperB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 395
 TomatoB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 391
 TobaccoB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 393
 MarigoldB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 393
 DaffodilB : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 403
 : SSNRIFLEETSIVARPGLRMEDIQERWARLKHIGTNVKRIEEDERCVTIPMGGLPVLQRVVGIGGTAGVWHPSTGYMVARTLAAARIVANAIVRYLGSPSSN : 396

FIG. 25B

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PotatoE	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 167						
ArabidopsisE	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 318						
AdonisE1	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 317						
AdonisE2	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 317						
LettuceEE	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 322						
TomatoE	YUNSKVDRIVEATNGHSI	VECEGDWV	IPCRFV	IVASGAASGK	FLQYEL	GGPRVSV	Q	TAYGV	VEVEN	IPDPS	UW	FMDYRDY	VRHDAQS	LEAKYPTFL	YAMPKSPTRVF	: 315						
PotatoE	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 276				
ArabidopsisE	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 422				
AdonisE1	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 427				
AdonisE1	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 427				
LettuceEE	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 431				
TomatoE	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 424				
MarigoldE	FEETCLASKDAMPFDLL	KKKULR	INTGVR	IRKE	EYEEENS	YIPVGGSL	PNT	EQKTL	AFGAAS	MWHPATGYS	VVRSLS	SEAPKCAF	AVL	ANIL	RQNH	SKMML	TSSSTPS-J	: 414				
PotatoE	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 378
ArabidopsisE	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 524
AdonisE1	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 529
AdonisE2	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 529
LettuceEE	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 533
TomatoE	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 526
MarigoldE	SITQAWNTLWPOE	RKRQRAF	FLFGIAL	IVQD	IEGIRSF	FRF	FRP	PKMA	QSG	FLGSS	LSX	ADLM	FAFYME	I	IAPND	MRQGL	IRHIL	LSDP	TGATL	IRTYL	TF	: 516

FIG. 26B

FIG. 25C

	*	460	*	480	*	500	*	520	*	540	*	
PotatoE	:	STPS-ISTQAWNTLW	POERKQORSFF	ELFGLALILQ	DI	EGERSF	FAFR	FRVPKVMQGF	GSSLSXADJ	MLFAFYMF	IAPNDMRRGLIRHLLSDPTGATLIRTYLTF--	: 378
ArabidopsisE	:	-----NISRQ	AWNTLWPERKQORAF	FLFGLALIVQ	FD	TGERSF	FR	TRFLPKVMQGF	GSSLTSGDL	VLFAFYMF	ISPNLKRGLINHLISDPTGATIMKTYLKV--	: 524
AdonisE1	:	SSAWNISMQ	AWSSLWPKERKQORAF	FLFGLLEIVQ	LD	ITRIF	FRT	FFRLPTVMQGF	GSSLSFSD	VLFSMYMFV	LAPNSMRMSLVRHLLSDPSGAVMVRAYLER--	: 529
AdonisE1	:	SSAWNISMQ	AWSSLWPKERKQORAF	FLFGLLEIVQ	LD	ITRIF	FRT	FFRLPTVMQGF	GSSLSFSD	VLFSMYMFV	LAPNSMRMSLVRHLLSDPSGAVMVKAYLER--	: 529
LettuceEE	:	KYT-NISKQ	AWETLWPERKQORAF	FLFGLSHIVMD	LEG	TRIF	FRT	FFRLPKVMQGF	GSSLSSTDL	ILFALYMFV	IAPHSLRMELVRHLLSDPTGATMVKAYLTI--	: 533
TomatoE	:	SSIPSISTQ	AWNTLWPOERKQORSFF	ELFGLALILQ	DI	EGERSF	FAFR	FRVPKVMQGF	GSSLSXADJ	MLFAFYMF	IAPNDMRKGLIRHLLSDPTGATLIRTYLTF--	: 526
MarigoldE	:	RYTTNISKQ	AWETLWPERKQORAF	FLFGLALIVQ	MD	IEGTRIF	FRT	FFRLPTVMQGF	GSSLSSTDL	ILFAYMF	IAPHSLRMGLVRHLLSDPTGGTMLKAYLTI--	: 516
ArabidopsisB	:	LRGQQLSAE	VMDLWPIERRRQREF	FCFGMDILL	KLD	ATRR	FD	AFDLQPHYMHG	FSSRLFI	PELVFGLSL	FSHASNTSRLEIMTK-GTVP-LAKMINNLVQDRO	: 501
AdonisB	:	-SGNELSAE	VAKOLWPIERRRQREF	FCFGMDILL	KLD	QSTR	FD	AFDLEPHYMHG	FSSRLFI	PELVFGLSL	FSHASNASRIEIMAK-GTVP-LVNMMNNLIPDID	: 502
PepperB	:	-SGDELSA	AVAKOLWPIERRRQREF	FCFGMDILL	KLD	IPATRR	FD	AFDLEPRVMHG	FSSRLFI	PELVFGLSL	FSHASNTSRLEIMTK-GTLP-LVHMNNLLQDKE	: 498
TomatoB	:	-SGNELSTA	VAKOLWPIERRRQREF	FCFGMDILL	KLD	IPATRR	FD	AFDLEPRVMHG	FSSRLFI	PELVFGLSL	FSHASNTSRFEIMTK-GTVP-LVNMINNLLQDKE	: 500
TobaccoB	:	-LGNELSA	AVAKOLWPIERRRQREF	FCFGMDILL	KLD	IPATRR	FD	AFDLEPRVMHG	FSSRLFI	PELVFGLSL	FSRASNTSRIEIMTK-GTLP-LVNMINNLLQDTE	: 500
MarigoldB	:	VTGD	LAAGVWRELWPIERRRQREF	FCFGMDILL	KLD	LEGTRR	FD	AFDLEPRVMHG	FSSRLFI	PELVTFGLS	FGHASNTCRVEIMAK-GTLP-LATMIGNLVRORE	: 511
Daffodi1B	:	-SGNDLSA	OVAKOLWPIERRRQREF	FCFGMDILL	KLD	LEGTRR	FD	AFDLEPRVMHG	FSSRLFI	PELVFPGLS	FSHASNTCKLEIMAK-GTLP-LVNMINNLLVQDRO	: 503

FIG. 26A

FIG. 20A

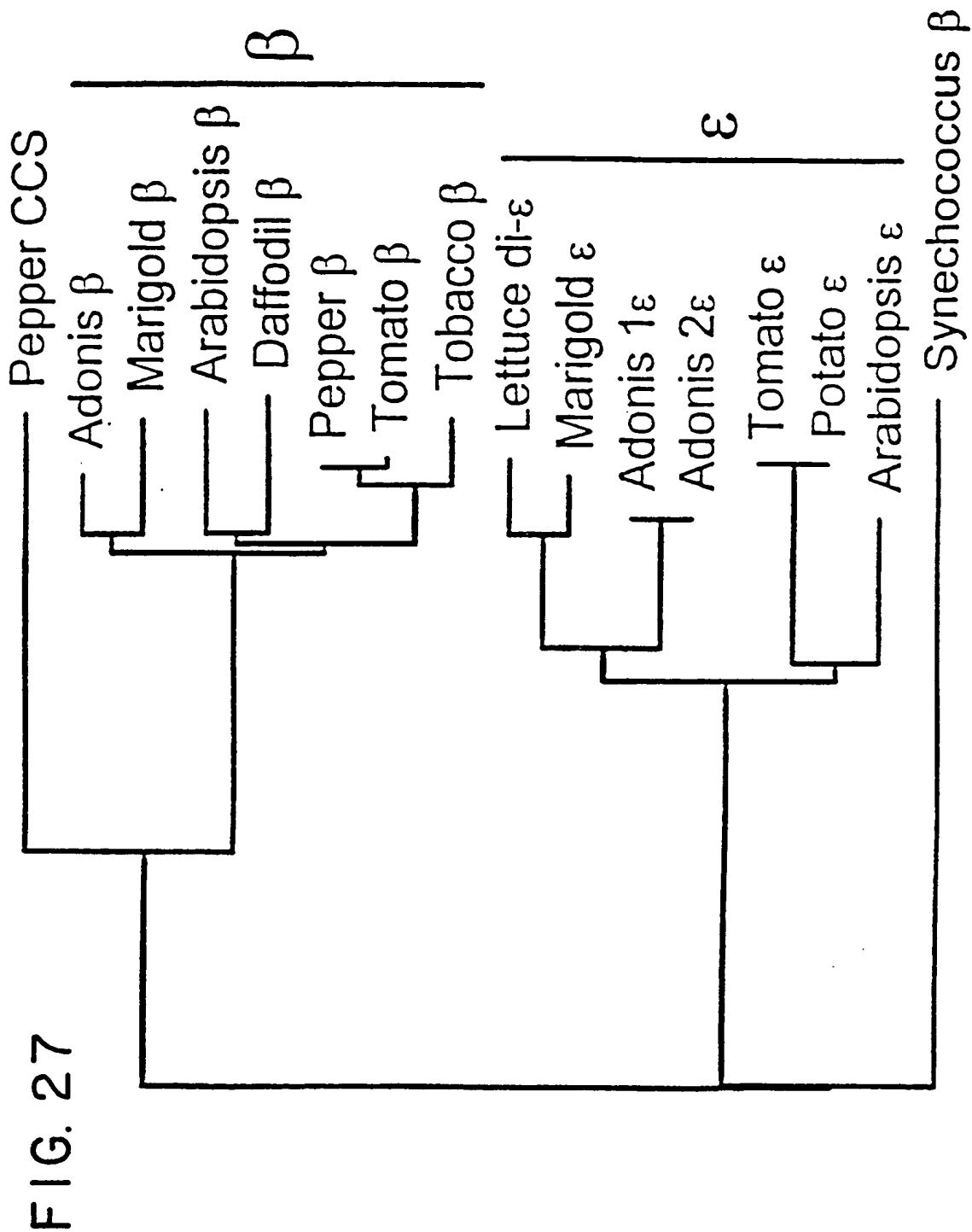
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PotatoE : -----
ArabidopsisE : MECVGARNF--AAMAVSTFPSWS--CRRKFPWKRVSRYNIRFGL--CSV--PASGGSSGSGSECVAVREDF--ADEEDFVAGGSELLFVQMQNQWDEQSKLVADKLEPPIS : 103
AdonisE1 : MELLGVRLN-----ISSCPVMT--FGTRNLSSSKLAYNITHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFVAGGSELLFVQMQQTIKSWEQAKLADKLEPPIP : 102
AdonisE2 : MELLGVRLN-----ISSCPVMT--FGTRNLSSSKLAYNITHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFVAGGSELLFVQMQQTIKSWEQAKLADKLEPPIP : 102
LettuceEE : MECFGARMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSA--SSSLRQIKCSAKSDR--CVWDQKQISVADIEEDVYVAGGSELLFVQMQRTIKSWEQSKLSEKLEQIP : 107
TomatoE : MECVGQNV--GAMAVLTRPLN-----RMSGGELCQEKSLFLAY--EQY--ESKCNSSSGSDSCVWDKEDF--ADEEDVYKAGGSQLVFVQMQNQWDEQSKLSELEQIS : 100
MarigoldE : MSMRAG--HMTATMAAFTCPRFM-----TSIRYT-----KQIKCNAKSO---LVVKQEI---EEEEEDVYKAGGSELLFVQMQNQWDEQSKLSEKLEPRVP : 84

```

[illegible]

43/45



44 / 45

FIG. 28A

GAP of: Arabidopsis epsilon cyclase to Lettuce epsilon cyclase

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1837	Length:	534
Ratio:	3.499	Gaps:	3
Percent Similarity:	76.381	Percent Identity:	69.905

Match display thresholds for the alignment(s):
 | = IDENTITY : = 2 . = 1

Arabidopsis x Lettuce

```

1  MECVGARNF.AAMAVSTFPSW...SCRRKFPVVKRYSYRNIRFGLCSVR 46
   ||| ||| | ||| | | . . | || ..| . : | :
1  MECFGARNMTATMAVFTCPRFTDCNIRHKFSLKQRRFTNLSASSSLRQI 50

47 SGGGSSGSESCVAVREDFADEEDFVKAGGSEILFVQMQQNKDMDEQSKLV 96
   | ||||:|||||: ||||. | |: |||
51 KCSAKSDRCVVDKQGISVADEEDYVKAGGSEFFVQMQRKSMESQSKLS 100

97 DKLPPISIGDGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLPTNN 146
   :|| | ||. || ||||| ||||| ||||| ||||| ||||| |||||
101 EKLAQIPIGNCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLPTNN 150

147 YGVWEDEFNDLGLQKCIHVVRETIVYLDLDDKPITIGRAYGRVSRLLHE 196
   ||||:||| |||: |||| |:|: |||| | | ||||| ||| ||||
151 YGVWQDEFI GLGLEGCIEHSWKDTLVYLDADPIRIGRAYGRVHRDLLHE 200

197 ELLRRCVESGVSYLSSKVDSITEASDGLRLVACDDNNAIPCRLATVASGA 246
   ||||| ||||| ||||: ||| . | |: |: | ||||| |||||
201 ELLRRCVESGVSYLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGA 250

247 ASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFM DYRDYTNEKV 296
   |||| |:|: ||||| ||||: ||||. |||| | ||||| ||| :. |
251 ASGKFLEYELGGPRVCVQTAYGIEVEVENNPYDPLMVFM DYRDFSKHKP 300

297 RSLEAEYPTFLYAMPMTKSRLFFEETCLASKDVPFDLLKTKMLRLDTL 346
   ||||. ||||| | |. :.: ||||| ||||: |||. |||. ||| | :
301 ESLEAKYPTFLYVMAMSPTKIFFEETCLASREAMPFNLLKSKLMSRLKAM 350

```

FIG. 28B

[illegible]

SEQUENCE LISTING

<110> CUNNINGHAM JR., FRANCIS X.
SUN, ZAIREN

<120> GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
METHODS OF USE THEREOF

<130> 8172-9023

<140> NOT YET ASSIGNED

<141> 1999-06-02

<150> 09/088,724

<151> 1998-06-02

<150> 09/088,725

<151> 1998-06-02

<160> 61

<170> PatentIn Ver. 2.0

<210> 1

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Met Glu Cys
1

GTT GGG GCT AGG AAT TTC GCA GCA ATG GCG GTT TCA ACA TTT CCG TCA 165
Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser
5 10 15

TGG AGT TGT CGA AGG AAA TTT CCA GTG GTT AAG AGA TAC AGC TAT AGG 213
Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg
20 25 30 35

AAT ATT CGT TTC GGT TTG TGT AGT GTC AGA GCT AGC GGC GGC GGA AGT 261
Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser
40 45 50

TCC GGT AGT GAG AGT TGT GTA GCG GTG AGA GAA GAT TTC GCT GAC GAA 309
Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu
55 60 65

GAA GAT TTT GTG AAA GCT GGT GGT TCT GAG ATT CTA TTT GTT CAA ATG 357
Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met
70 75 80

CAG CAG AAC AAA GAT ATG GAT GAA CAG TCT AAG CTT GTT GAT AAG TTG 405

Gln	Gln	Asn	Lys	Asp	Met	Asp	Glu	Gln	Ser	Lys	Leu	Val	Asp	Lys	Leu	
	85					90					95					
CCT	CCT	ATA	TCA	ATT	GGT	GAT	GGT	GCT	TTG	GAT	CAT	GTG	GTT	ATT	GGT	453
Pro	Pro	Ile	Ser	Ile	Gly	Asp	Gly	Ala	Leu	Asp	His	Val	Val	Ile	Gly	
100					105					110					115	
TGT	GGT	CCT	GCT	GGT	TTA	GCC	TTG	GCT	GCA	GAA	TCA	GCT	AAG	CTT	GGA	501
Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly	
				120				125						130		
TTA	AAA	GTT	GGA	CTC	ATT	GGT	CCA	GAT	CTT	CCT	TTT	ACT	AAC	AAT	TAC	549
Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	
			135				140						145			
GGT	GTT	TGG	GAA	GAT	GAA	TTC	AAT	GAT	CTT	GGG	CTG	CAA	AAA	TGT	ATT	597
Gly	Val	Trp	Glu	Asp	Glu	Phe	Asn	Asp	Leu	Gly	Leu	Gln	Lys	Cys	Ile	
	150						155					160				
GAG	CAT	GTT	TGG	AGA	GAG	ACT	ATT	GTG	TAT	CTG	GAT	GAT	GAC	AAG	CCT	645
Glu	His	Val	Trp	Arg	Glu	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Lys	Pro	
	165					170					175					
ATT	ACC	ATT	GGC	CGT	GCT	TAT	GGA	AGA	GTT	AGT	CGA	CGT	TTG	CTC	CAT	693
Ile	Thr	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	Arg	Leu	Leu	His	
180					185					190					195	
GAG	GAG	CTT	TTG	AGG	AGG	TGT	GTC	GAG	TCA	GGT	GTC	TCG	TAC	CTT	AGC	741
Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Ser	
				200				205						210		
TCG	AAA	GTT	GAC	AGC	ATA	ACA	GAA	GCT	TCT	GAT	GGC	CTT	AGA	CTT	GTT	789
Ser	Lys	Val	Asp	Ser	Ile	Thr	Glu	Ala	Ser	Asp	Gly	Leu	Arg	Leu	Val	
			215					220					225			
GCT	TGT	GAC	GAC	AAT	AAC	GTC	ATT	CCC	TGC	AGG	CTT	GCC	ACT	GTT	GCT	837
Ala	Cys	Asp	Asp	Asn	Asn	Val	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	
	230					235						240				
TCT	GGA	GCA	GCT	TCG	GGA	AAG	CTC	TTG	CAA	TAC	GAA	GTT	GGT	GGA	CCT	885
Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr		Glu	Val	Gly	Pro	
	245					250					255					
AGA	GTC	TGT	GTG	CAA	ACT	GCA	TAC	GGC	GTG	GAG	GTT	GAG	GTG	GAA	AAT	933
Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	
260					265					270					275	
AGT	CCA	TAT	GAT	CCA	GAT	CAA	ATG	GTT	TTC	ATG	GAT	TAC	AGA	GAT	TAT	981
Ser	Pro	Tyr	Asp	Pro	Asp	Gln	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	
				280					285					290		
ACT	AAC	GAG	AAA	GTT	CGG	AGC	TTA	GAA	GCT	GAG	TAT	CCA	ACG	TTT	CTG	1029
Thr	Asn	Glu	Lys	Val	Arg	Ser	Leu	Glu	Ala	Glu	Tyr	Pro	Thr	Phe	Leu	
			295					300					305			
TAC	GCC	ATG	CCT	ATG	ACA	AAG	TCA	AGA	CTC	TTC	TTC	GAG	GAG	ACA	TGT	1077
Tyr	Ala	Met	Pro	Met	Thr	Lys	Ser	Arg	Leu	Phe	Phe	Glu	Glu	Thr	Cys	
	310						315					320				
TTG	GCC	TCA	AAA	GAT	GTC	ATG	CCC	TTT	GAT	TTG	CTA	AAA	ACG	AAG	CTC	1125
Leu	Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	Thr	Lys	Leu	

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GAG GAG TGG TCC TAT ATC CCA GTT GGT GGT TCC TTG CCA AAC ACC GAA Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu 360 365 370			1221
CAA AAG AAT CTC GCC TTT GGT GCT GCC GCT AGC ATG GTA CAT CCC GCA Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala 375 380 385			1269
ACA GGC TAT TCA GTT GTG AGA TCT TTG TCT GAA GCT CCA AAA TAT GCA Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala 390 395 400			1317
TCA GTC ATC GCA GAG ATA CTA AGA GAA GAG ACT ACC AAA CAG ATC AAC Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn 405 410 415			1365
AGT AAT ATT TCA AGA CAA GCT TGG GAT ACT TTA TGG CCA CCA GAA AGG Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg 420 425 430 435			1413
AAA AGA CAG AGA GCA TTC TTT CTC TTT GGT CTT GCA CTC ATA GTT CAA Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln 440 445 450			1461
TTC GAT ACC GAA GGC ATT AGA AGC TTC TTC CGT ACT TTC TTC CGC CTT Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu 455 460 465			1509
CCA AAA TGG ATG TGG CAA GGG TTT CTA GGA TCA ACA TTA ACA TCA GGA Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly 470 475 480			1557
GAT CTC GTT CTC TTT GCT TTA TAC ATG TTC GTC ATT TCA CCA AAC AAT Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn 485 490 495			1605
TTG AGA AAA GGT CTC ATC AAT CAT CTC ATC TCT GAT CCA ACC GGA GCA Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala 500 505 510 515			1653
ACC ATG ATA AAA ACC TAT CTC AAA GTA TGATTTACTT ATCAACTCTT Thr Met Ile Lys Thr Tyr Leu Lys Val 520			1700
AGGTTTGTGT ATATATATGT TGATTTATCT GAATAATCGA TCAAAGAATG GTATGTGGGT			1760
TACTAGGAAG TTGGAACAA ACATGTATAG AATCTAAGGA GTGATCGAAA TGGAGATGGA			1820
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 50 55 60
 Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
 65 70 75 80
 Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
 85 90 95
 Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
 100 105 110
 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
 115 120 125
 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
 130 135 140
 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
 145 150 155 160
 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
 165 170 175
 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
 180 185 190
 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
 195 200 205
 Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
 210 215 220
 Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
 225 230 235 240
 Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
 245 250 255
 Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
 260 265 270
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 Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
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 Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
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Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
 325 330 335
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 340 345 350
 Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
 355 360 365
 Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
 370 375 380
 His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
 385 390 395 400
 Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
 405 410 415
 Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
 420 425 430
 Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
 435 440 445
 Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
 450 455 460
 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
 465 470 475 480
 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
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AGAATTCTCC GATTGAGAAC GATGAGAGAC CGGAGAGCAC GAGCTCCACA AACGCTATAG	180
ACGCTGAGTA TCTGGCGTTG CGTTTGCGG AGAAATTGGA GAGGAAGAAA TCGGAGAGGT	240
CCACTTATCT AATCGCTGCT ATGTTGTCGA GCTTTGGTAT CACTTCTATG GCTGTTATGG	300
CTGTTTACTA CAGATTCTCT TGGCAAATGG AGGGAGGTGA GATCTCAATG TTGGAAATGT	360
TTGGTACATT TGCTCTCTCT GTTGGTGCTG CTGTTGGTAT GGAATTCTGG GCAAGATGGG	420
CTCATAGAGC TCTGTGGCAC GCTTCTCTAT GGAATATGCA TGAGTCACAT CACAAACCAA	480

GAGAAGGACC GTTTGAGCTA AACGATGTTT TTGCTATAGT GAACGCTGGT CCAGCGATTG 540
 GTCTCCTCTC TTATGGATTC TTCAATAAAG GACTCGTTCC TGGTCTCTGC TTTGGCGCCG 600
 GGTTAGGCAT AACGGTGTTT GGAATCGCCT ACATGTTTGT CCACGATGGT CTCGTGCACA 660
 AGCGTTTCCC TGTAGGTCCC ATCGCCGACG TCCCTTACCT CCGAAAGGTC GCCGCCGCTC 720
 ACCAGCTACA TCACACAGAC AAGTTCAATG GTGTACCATA TGGACTGTTT CTTGGACCCA 780
 AGGAATTGGA AGAAGTTGGA GGAAATGAAG AGTTAGATAA GGAGATTAGT CGGAGAATCA 840
 AATCATACAA AAAGGCCTCG GGCTCCGGGT CGAGTTCGAG TTCTTGACTT TAAACAAGTT 900
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 35 40 45
 Arg Pro Glu Ser Thr Ser Ser Thr Asn Ala Ile Asp Ala Glu Tyr Leu
 50 55 60
 Ala Leu Arg Leu Ala Glu Lys Leu Glu Arg Lys Lys Ser Glu Arg Ser
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 Thr Tyr Leu Ile Ala Ala Met Leu Ser Ser Phe Gly Ile Thr Ser Met
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 Ala Val Met Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly
 100 105 110
 Glu Ile Ser Met Leu Glu Met Phe Gly Thr Phe Ala Leu Ser Val Gly
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 Trp His Ala Ser Leu Trp Met Asn His Glu Ser His His Lys Pro Arg
 145 150 155 160
 Glu Gly Pro Phe Glu Leu Asn Asp Val Phe Ala Ile Val Asn Ala Gly
 165 170 175
 Pro Ala Ile Gly Leu Leu Ser Tyr Gly Phe Phe Asn Lys Gly Leu Val
 180 185 190
 Pro Gly Leu Cys Phe Gly Ala Gly Leu Gly Ile Thr Val Phe Gly Ile
 195 200 205

Ala Tyr Met Phe Val His Asp Gly Leu Val His Lys Arg Phe Pro Val
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 Gly Pro Ile Ala Asp Val Pro Tyr Leu Arg Lys Val Ala Ala Ala His
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 Gln Leu His His Thr Asp Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe
 245 250 255
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 Gly Ser Ser Ser Ser Ser
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 35 40 45
 Asn Asp Leu Tyr Gly Val Val Phe Ala Val Leu Ala Thr Ile Leu Phe
 50 55 60
 Thr Val Gly Ala Tyr Trp Trp Pro Val Leu Trp Trp Ile Ala Leu Gly
 65 70 75 80
 Met Thr Val Tyr Gly Leu Ile Tyr Phe Ile Leu His Asp Gly Leu Val
 85 90 95
 His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Arg Gly Tyr Phe Arg
 100 105 110
 Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
 115 120 125
 His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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 Lys Gln Asp Leu Lys Arg Ser Gly Val Leu Arg Pro Gln Asp Glu Arg
 145 150 155 160
 Pro Ser

<210> 6
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<400> 6
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Ile Ala Ala Phe Thr His Arg Tyr Ile Met His Gly Trp Gly Trp Arg
20 25 30
Trp His Glu Ser His His Thr Pro Arg Lys Gly Val Phe Glu Leu Asn
35 40 45
Asp Leu Phe Ala Val Val Phe Ala Gly Val Ala Ile Ala Leu Ile Ala
50 55 60
Val Gly Thr Ala Gly Val Trp Pro Leu Gln Trp Ile Gly Cys Gly Met
65 70 75 80
Thr Val Tyr Gly Leu Leu Tyr Phe Leu Val His Asp Gly Leu Val His
85 90 95
Gln Arg Trp Pro Phe His Trp Ile Pro Arg Arg Gly Tyr Leu Lys Arg
100 105 110
Leu Tyr Val Ala His Arg Leu His His Ala Val Arg Gly Arg Glu Gly
115 120 125
Cys Val Ser Phe Gly Phe Ile Tyr Ala Arg Lys Pro Ala Asp Leu Gln
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Ala Ile Leu Arg Glu Arg His Gly Arg Pro Pro Lys Arg Asp Ala Ala
145 150 155 160
Lys Asp Arg Pro Asp Ala Ala Ser Pro Ser Ser Ser Pro Glu
165 170 175

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Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
50 55 60
Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
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Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
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 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
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<210> 8
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 <212> PRT
 <213> Agrobacterium aurianticum

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 35 40 45
 Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
 50 55 60
 Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
 65 70 75 80
 Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
 85 90 95
 His Trp Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
 100 105 110
 Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
 115 120 125
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 Arg Thr

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 <211> 954
 <212> DNA
 <213> Arabidopsis thaliana

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TGGGACATGA	CACTAAGTAT	AACTGTCATC	TGATGGAAAA	GATTGAAGCT	GAGAATTTAC	240
TTCACAGAGC	TTTCAGTGTG	TTTTTATTCA	ACTCCAAGTA	TGAGTTGCTT	CTCCAGCAAC	300
GGTCAAAAAC	AAAGGTTACT	TTCCCACTTG	TGTGGACAAA	CACTTGTTGC	AGCCATCCTC	360
TTTACCGTGA	ATCCGAGCTT	ATTGAAGAGA	ATGTGCTTGG	TGTAAGAAAT	GCCGCACAAA	420
GGAAGCTTTT	CGATGAGCTC	GGTATTGTAG	CAGAAGATGT	ACCAGTCGAT	GAGTTCCTC	480
CCTTGGGACG	CATGCTTTAC	AAGGCACCTT	CTGATGGGAA	ATGGGGAGAG	CACGAAGTTG	540
ACTATCTACT	CTTCATCGTG	CGGGATGTGA	AGCTTCAACC	AAACCCAGAT	GAAGTGGCTG	600
AGATCAAGTA	CGTGAGCAGG	GAAGAGCTTA	AGGAGCTGGT	GAAGAAAGCA	GATGCTGGCG	660
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GGTGGGATCA	TGTTGAGAAA	GGAACATCA	CTGAAGCTGC	AGACATGAAA	ACCATTACACA	780
AGCTCTGAAC	TTTCCATAAG	TTTTGGATCT	TCCCTTCCC	ATAATAAAAT	TAAGAGATGA	840
GACTTTTATT	GATTACAGAC	AAAACTGGCA	ACAAAATCTA	TTCCTAGGAT	TTTTTTTTGC	900
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<210> 10

<211> 996

<212> DNA

<213> *Arabidopsis thaliana*

<400> 10

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GAAAGTTACC	GAATTTTCGT	GCTTCTCTG	GTACCGCTAT	GACAGATACT	AAAGATGCTG	180
GTATGGATGC	TGTTTCAGAGA	CGTCTCATGT	TTGAGGATGA	ATGCATTCTT	GTTGATGAAA	240
CTGATCGTGT	TGTGGGGCAT	GTCAGCAAGT	ATAATTGTCA	TCTGATGGAA	AATATTGAAG	300
CCAAGAATTT	GCTGCACAGG	GCTTTTAGTG	TATTTTTATT	CAACTCGAAG	TATGAGTTGC	360
TTCTCCAGCA	AAGGTCAAAC	ACAAAGGTTA	CGTTCCCTCT	AGTGTGGACT	AACACTTGTT	420
GCAGCCATCC	TCTTTACCGT	GAATCAGAGC	TTATCCAGGA	CAATGCACTA	GGTGTGAGGA	480
ATGCTGCACA	AAGAAAGCTT	CTCGATGAGC	TTGGTATTGT	AGCTGAAGAT	GTACCAGTCG	540
ATGAGTTCAC	TCCCTTGGGA	CGTATGCTGT	ACAAGGCTCC	TTCTGATGGC	AAATGGGGAG	600
AGCATGAACT	TGATTACTTG	CTCTTCATCG	TGCGAGACGT	GAAGGTTCAA	CCAAACCCAG	660
ATGAAGTAGC	TGAGATCAAG	TATGTGAGCC	GGGAAGAGCT	GAAGGAGCTG	GTGAAGAAAG	720
CAGATGCAGG	TGAGGAAGGT	TTGAAACTGT	CACCATGGTT	CAGATTGGTG	GTGGACAATT	780

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AAACCATCCA CAAACTCTGA ACATCTTTTT TTAAAGTTTT TAAATCAATC AACTTTCTCT	900
TCATCATTTT TATCTTTTCG ATGATAATAA TTTGGGATAT GTGAGACACT TACAAAACCT	960
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<210> 11

<211> 1165

<212> DNA

<213> Haematococcus pluvialis

<400> 11

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CCAGCTGTGC ACACGCGCGA CTCCAGTTTA AGCTCAGGAG CATGCAGATG ACGCTCATGC	180
AGCCCAGCAT CTCAGCCAAT CTGTCGCGCG CCGAGGACCG CACAGACCAC ATGAGGGGTG	240
CAAGCACCTG GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT	300
TGGTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGAGTGT CACAAGTTCC	360
TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC TGTGTTCTTG TTTGACGATC	420
AGGGGCGACT GCTGCTGCAA CAGCGTGCAC GCTCAAAAAT CACCTTCCCA AGTGTGTGGA	480
CGAACACCTG CTGCAGCCAC CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA	540
GCCAGGTGGC CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC	600
ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC CTCACGCGTT	660
TGCACTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA ATCAGCGCTC TGGGGCGAGC	720
ACGAAATGGA CTACATCTTG TTCATCCGGG CCAACGTCAC CTTGGCGCCC AACCCTGACG	780
AGGTGGACGA AGTCAGGTAC GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA	840
ACGGGCTGCA ATGGTCGCCG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT	900
GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA ACGGTGCATC	960
ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA GACACGTCAT GGGGTGGAAT	1020
TGCGTACTTG GCAGCTTCGT ATCTCCTTTT TCTGAGACTG AACCTGCAGT CAGGTCCCAC	1080
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<210> 12

<211> 1135

<212> DNA

<213> Haematococcus pluvialis

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 CCAGCTGTGC ACACGCGCGA CTCCAGTTTA AGCTCAGGAG CATGCAGCTG CTTTCCGAGG 180
 ACCGCACAGA CCACATGAGG GGTGCAAGCA CCTGGGCAGG CGGGCAGTCG CAGGATGAGC 240
 TGATGCTGAA GGACGAGTGC ATCTTGGTAG ATGTTGAGGA CAACATCACA GGCCATGCCA 300
 GCAAGCTGGA GTGTCACAAG TTCCTACCAC ATCAGCCTGC AGGCCTGCTG CACCGGGCCT 360
 TCTCTGTGTT CCTGTTTGAC GATCAGGGGC GACTGCTGCT GCAACAGCGT GCACGCTCAA 420
 AAATCACCTT CCCAAGTGTG TGGACGAACA CCTGCTGCAG CCACCCTTTA CATGGGCAGA 480
 CCCCAGATGA GGTGGACCAA CTAAGCCAGG TGGCCGACGG AACAGTACCT GGCGCAAAGG 540
 CTGCTGCCAT CCGCAAGTTG GAGCACGAGC TGGGGATACC AGCGCACCAG CTGCCGGCAA 600
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 CACAATCAGC GCTCTGGGGC GAGCACGAAA TGGACTACAT CTTGTTTCATC CGGGCCAACG 720
 TCACCTTGGC GCCCAACCCT GACGAGGTGG ACGAAGTCAG GTACGTGACG CAAGAGGAGC 780
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 ACGAGGATTG GGGAACGGTG CATCACATCA ACGAAGCGTG AAGGCAGAAG CTGCAGGATG 960
 TGAAGACACG TCATGGGGTG GAATTGCGTA CTTGGCAGCT TCGTATCTCC TTTTCTGAG 1020
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<210> 13
 <211> 960
 <212> DNA
 <213> Tagetes erecta

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 GTAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAATAC GAGTTACTTC 240
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 GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAC GCCTGAGAGA ATGCTGCACA 360
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 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 480

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TGAAAACCAT ACACAAGCTG ATATAGAAAC ACACCCCTCAA CCGAAAAGCA AGCCTAATAA 780
TTCGGGTTGG GTCGGGTCTA CCATCAATTG TTTTCTTCTT TTAACAACCTT TTAATCTCTA 840
TTTGAGCATG TTGATTCTTG TCTTTTGTGT GTAAGATTTT GGGTTTCGTT TCAGTTGTAA 900
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<210> 14

<211> 305

<212> PRT

<213> Haematococcus pluvialis

<400> 14

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      20           25           30

Arg Ser Met Gln Met Thr Leu Met Gln Pro Ser Ile Ser Ala Asn Leu
      35           40           45

Ser Arg Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp
      50           55           60

Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile
      65           70           75           80

Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala Ser Lys Leu Glu
      85           90           95

Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu Leu His Arg Ala
      100          105          110

Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln
      115          120          125

Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn Thr Cys
      130          135          140

Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp Gln Leu
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Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala Ala Ile
      165          170          175

Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu Pro Ala
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Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val
      195          200          205

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Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp
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 Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp
 225 230 235 240
 Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met
 245 250 255
 Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile
 260 265 270
 Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala Ala Leu
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 Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile Asn Glu
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Ala
 305

<210> 15
 <211> 293
 <212> PRT
 <213> Haematococcus pluvialis

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 35 40 45
 Ala Ser Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys
 50 55 60
 Asp Glu Cys Ile Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala
 65 70 75 80
 Ser Lys Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu
 85 90 95
 Leu His Arg Ala Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu
 100 105 110
 Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp
 115 120 125
 Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu
 130 135 140
 Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys
 145 150 155 160
 Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His
 165 170 175
 Gln Leu Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys

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His	Glu	Met	Asp	Tyr	Ile	Leu	Phe	Ile	Arg	Ala	Asn	Val	Thr	Leu	Ala
	210					215					220				
Pro	Asn	Pro	Asp	Glu	Val	Asp	Glu	Val	Arg	Tyr	Val	Thr	Gln	Glu	Glu
225					230					235					240
Leu	Arg	Gln	Met	Met	Gln	Pro	Asp	Asn	Gly	Leu	Gln	Trp	Ser	Pro	Trp
				245					250					255	
Phe	Arg	Ile	Ile	Ala	Ala	Arg	Phe	Leu	Glu	Arg	Trp	Trp	Ala	Asp	Leu
			260					265					270		
Asp	Ala	Ala	Leu	Asn	Thr	Asp	Lys	His	Glu	Asp	Trp	Gly	Thr	Val	His
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His	Ile	Asn	Glu	Ala											
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<213> Arabidopsis thaliana															
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			20					25					30		
Leu	Ser	Ser	Ile	Ser	Pro	Arg	Lys	Leu	Pro	Asn	Phe	Arg	Ala	Phe	Ser
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Gly	Thr	Ala	Met	Thr	Asp	Thr	Lys	Asp	Ala	Gly	Met	Asp	Ala	Val	Gln
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Arg	Arg	Leu	Met	Phe	Glu	Asp	Glu	Cys	Ile	Leu	Val	Asp	Glu	Thr	Asp
	65				70					75					80
Arg	Val	Val	Gly	His	Val	Ser	Lys	Tyr	Asn	Cys	His	Leu	Met	Glu	Asn
				85					90					95	
Ile	Glu	Ala	Lys	Asn	Leu	Leu	His	Arg	Ala	Phe	Ser	Val	Phe	Leu	Phe
			100					105					110		
Asn	Ser	Lys	Tyr	Glu	Leu	Leu	Leu	Gln	Gln	Arg	Ser	Asn	Thr	Lys	Val
		115					120					125			
Thr	Phe	Pro	Leu	Val	Trp	Thr	Asn	Thr	Cys	Cys	Ser	His	Pro	Leu	Tyr
	130					135					140				
Arg	Glu	Ser	Glu	Leu	Ile	Gln	Asp	Asn	Ala	Leu	Gly	Val	Arg	Asn	Ala
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Ala	Gln	Arg	Lys	Leu	Leu	Asp	Glu	Leu	Gly	Ile	Val	Ala	Glu	Asp	Val
				165					170					175	

Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
 180 185 190
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
 195 200 205
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
 210 215 220
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
 225 230 235 240
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
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 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
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<210> 17

<211> 287

<212> PRT

<213> Clarkia breweri

<400> 17

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 Ser Ser Gln Ala Thr Thr Met Gly Glu Val Val Asp Ala Gly Met Asp
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 Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp
 65 70 75 80
 Glu Asn Asp Lys Val Val Gly His Glu Ser Lys Tyr Asn Cys His Leu
 85 90 95
 Met Glu Lys Ile Glu Ser Glu Asn Leu Leu His Arg Ala Phe Ser Val
 100 105 110
 Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala
 115 120 125
 Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His
 130 135 140
 Pro Leu Tyr Arg Glu Ser Glu Leu Ile Asp Glu Asn Cys Leu Gly Val
 145 150 155 160
 Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala
 165 170 175
 Glu Asp Leu Pro Val Asp Gln Phe Ile Pro Leu Ser Arg Ile Leu Tyr

180	185	190
Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu		
195	200	205
Leu Phe Ile Ile Arg Asp Val Asn Leu Asp Pro Asn Pro Asp Glu Val		
210	215	220
Ala Glu Val Lys Tyr Met Asn Arg Asp Asp Leu Lys Glu Leu Leu Arg		
225	230	235
Lys Ala Asp Ala Glu Glu Gly Val Lys Leu Ser Pro Trp Phe Arg		
245	250	255
Leu Val Val Asp Asn Phe Leu Phe Lys Trp Trp Asp His Val Glu Lys		
260	265	270
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275	280	285

<210> 18

<211> 261

<212> PRT

<213> Arabidopsis thaliana

<400> 18

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Glu Cys Ile Leu Val Asp Glu Asn Asn Arg Val Val Gly His Asp Thr	
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Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala Glu Asn Leu Leu	
65	70
His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu	
85	90
Leu Gln Gln Arg Ser Lys Thr Lys Val Thr Phe Pro Leu Val Trp Thr	
100	105
Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Glu	
115	120
Glu Asn Val Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu Phe Asp	
130	135
Glu Leu Gly Ile Val Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro	
145	150
Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu	
165	170
His Glu Val Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Lys Leu Gln	
180	185
	190

Pro Asn Pro Asp Glu Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu
 195 200 205
 Leu Lys Glu Leu Val Lys Lys Ala Asp Ala Gly Asp Glu Ala Val Lys
 210 215 220
 Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp
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 Trp Asp His Val Glu Lys Gly Thr Ile Thr Glu Ala Ala Asp Met Lys
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 Thr Ile His Lys Leu
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<210> 19

<211> 288

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 19

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 35 40 45
 Thr Ser Asn Asp Glu Ser Gly Glu Thr Cys Phe Ser Gly His Asp Glu
 50 55 60
 Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp Asp
 65 70 75 80
 Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met Glu
 85 90 95
 Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile Phe
 100 105 110
 Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu Lys Ile
 115 120 125
 Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
 130 135 140
 Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys
 145 150 155 160
 Gly Ala Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile
 165 170 175
 Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg
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Lys	Ser	Ser 35	Ala	Leu	Leu	Glu	Leu 40	Val	Pro	Glu	Thr	Lys 45	Lys	Glu	Asn
Leu	Asp 50	Phe	Glu	Leu	Pro	Met 55	Tyr	Asp	Pro	Ser	Lys 60	Gly	Val	Val	Asp
Leu 65	Ala	Val	Val	Gly	Gly 70	Gly	Pro	Ala	Gly	Leu 75	Ala	Val	Ala	Gln	Gln 80
Val	Ser	Glu	Ala	Gly 85	Leu	Ser	Val	Cys	Ser 90	Ile	Asp	Pro	Pro	Lys 95	Leu
Ile	Trp	Pro	Asn 100	Asn	Tyr	Gly	Val	Trp 105	Val	Asp	Glu	Phe	Glu 110	Ala	Met
Asp	Leu	Leu 115	Asp	Cys	Leu	Asp	Ala 120	Thr	Trp	Ser	Gly	Ala 125	Val	Tyr	Ile
Asp	Asp 130	Thr	Lys	Asp	Leu	Arg 135	Pro	Tyr	Gly	Arg	Val 140	Asn	Arg	Lys	Gln
Leu 145	Lys	Ser	Lys	Met	Met 150	Gln	Lys	Cys	Ile	Asn 155	Gly	Val	Lys	Phe	His 160
Gln	Ala	Lys	Val	Ile 165	Lys	Val	Ile	His	Glu 170	Glu	Lys	Ser	Met	Leu 175	Ile
Cys	Asn	Asp	Gly 180	Thr	Ile	Gln	Ala	Thr 185	Val	Val	Leu	Asp	Ala 190	Thr	Gly
Phe	Ser	Arg	Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln

195					200					205					
Val	Ala	Tyr	Gly	Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Lys
210						215					220				
Met	Val	Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Asn	Asn	Glu	Leu	Lys
225					230					235					240
Glu	Arg	Asn	Ser	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Ser	Ser
				245					250					255	
Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	Gly	Leu
			260					265					270		
Arg	Met	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	His	Leu	Gly
		275					280					285			
Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	Val	Ile	Pro	Met
290						295					300				
Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	Ile	Gly	Gly
305					310					315					320
Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	Arg	Thr
				325					330					335	
Leu	Ala	Ala	Ala	Pro	Val	Val	Ala	Asn	Ala	Ile	Ile	Tyr	Leu	Gly	Ser
			340					345					350		
Glu	Ser	Ser	Gly	Glu	Leu	Ser	Ala	Glu	Val	Trp	Lys	Asp	Leu	Trp	Pro
		355					360					365			
Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile
370					375					380					
Leu	Leu	Lys	Leu	Asp	Leu	Pro	Ala	Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe
385					390					395					400
Phe	Asp	Leu	Glu	Pro	Arg	Tyr	Trp	His	Gly	Phe	Leu	Ser	Ser	Arg	Leu
				405					410					415	
Phe	Leu	Pro	Glu	Leu	Ile	Val	Phe	Gly	Leu	Ser	Leu	Phe	Ser	His	Ala
			420					425					430		
Ser	Asn	Thr	Ser	Arg	Glu	Ile	Met	Thr	Lys	Gly	Thr	Pro	Leu	Val	Met
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Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
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 Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
 50 55 60
 Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
 65 70 75 80
 Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
 85 90 95
 Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
 100 105 110
 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
 115 120 125
 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
 130 135 140
 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
 145 150 155 160
 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
 165 170 175
 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
 180 185 190
 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
 195 200 205
 Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
 210 215 220
 Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
 225 230 235 240
 Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
 245 250 255
 Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
 260 265 270
 Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
 275 280 285
 Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
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 Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
 305 310 315 320
 Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
 325 330 335
 Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
 340 345 350
 Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro

355 360 365
 Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
 370 375 380
 His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
 385 390 395 400
 Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
 405 410 415
 Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
 420 425 430
 Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
 435 440 445
 Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
 450 455 460
 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
 465 470 475 480
 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
 485 490 495
 Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
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 Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
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<210> 22

<211> 1898

<212> DNA

<213> Adonis palaestina

<400> 22

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 ACTTGGTGTG CGCAACCTCA TCTCTTCTTG CCCTGTGTGG ACTTTTGGAA CAAGAAACCT 180
 TAGTAGTTCA AACTAGCTT ATAACATACA TCGATATGGT TCTTCTTGTA GAGTAGATTT 240
 TCAAGTGAGA GCTGATGGTG GAAGCGGGAG TAGAAGTTCT GTTGCTTATA AAGAGGGTTT 300
 TGTGGATGAA GAGGATTTTA TCAAAGCTGG TGGTTCTGAG CTTTGTGTTG TCCAAATGCA 360
 GCAAACAAAG TCTATGGAGA AACAGGCCAA GCTCGCCGAT AAGTTGCCAC CAATACCTTT 420
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 TGCAGAAGCT GCTAAGCTAG GGTGAAAGT TGGCCTTATT GGTCTGATC TTCCTTTTAC 540
 AAATAATTAT GGTGTGTGGG AAGACGAGTT CAAAGATCTT GGAATTGAAC GTTGATCGA 600
 GCATGCTTGG AAGGACACCA TCGTATATCT TGATAATGAT GCTCCTGTCC TTATTGGTCG 660
 TGCATATGGA CGAGTTAGTC GACATTTGCT ACATGAGGAG TTGCTGAAAA GGTGTGTGGA 720

GTCAGGTGTA TCATATCTTG ATTCTAAAGT GGAAAGGATC ACTGAAGCTG GTGATGGCCA 780
 TAGCCTTGTA GTTTGTGAAA ATGAGATCTT TATCCCTTGC AGGCTTGCTA CTGTTGCATC 840
 TGGAGCAGCT TCAGGGGAAAC TTTTGGAGTA TGAAGTAGGT GGCCCTCGTG TTTGTGTCCA 900
 AACCGCTTAT GGGGTGGAGG TTGAGGTGGA GAACAATCCA TACGATCCCA ACTTAATGGT 960
 ATTCATGGAC TACAGAGACT ATATGCAACA GAAATTACAG TGCTCGGAAG AAGAATATCC 1020
 AACATTTCTC TATGTCATGC CCATGTCGCC AACAAGACTT TTTTTTGAGG AAACCTGTTT 1080
 GGCCTCAAAA GATGCCATGC CATTGATCT ACTGAAGAGA AAACCTGATGT CACGATTGAA 1140
 GACTCTGGGT ATCCAAGTTA CAAAAGTTTA TGAAGAGGAA TGGTCATATA TTCCTGTTGG 1200
 TGGTTCTTTA CCAAACACAG AGCAAAAGAA CCTAGCATTT GGTGCTGCAG CAAGCATGGT 1260
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 TGTAATTGCA AAGATTTTGA AGCAAGATAA CTCTGCGTAT GTGGTTTCTG GACAAAGTAG 1380
 TGCAGTAAAC ATTTCAATGC AAGCATGGAG CAGTCTTTGG CCAAAGGAGC GAAAACGTCA 1440
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 AAGAGCTTAC CTCGAAAGGT AGTCTCATCT ATTATTAAAC TCTAGTGTTT CACCAAATAA 1740
 ATGAGGATCC TTCGAATGTG TATATGATCA TCTCTATGTA TATCCTGTAC TCTAATCTCA 1800
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<211> 529

<212> PRT

<213> Adonis palaestina

<400> 23

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His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
 35 40 45

Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
 50 55 60

Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
 65 70 75 80

Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
 85 90 95
 Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
 100 105 110
 Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
 115 120 125
 Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
 130 135 140
 Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
 145 150 155 160
 Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
 165 170 175
 Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
 180 185 190
 Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
 195 200 205
 Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
 210 215 220
 Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr
 225 230 235 240
 Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
 245 250 255
 Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
 260 265 270
 Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
 275 280 285
 Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
 290 295 300
 Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
 305 310 315 320
 Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
 325 330 335
 Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
 340 345 350
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 355 360 365
 Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
 370 375 380
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
 385 390 395 400
 Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr

405								410				415			
Val	Val	Ser	Gly	Gln	Ser	Ser	Ala	Val	Asn	Ile	Ser	Met	Gln	Ala	Trp
			420						425				430		
Ser	Ser	Leu	Trp	Pro	Lys	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu
		435					440					445			
Phe	Gly	Leu	Glu	Leu	Ile	Val	Gln	Leu	Asp	Ile	Glu	Ala	Thr	Arg	Thr
	450					455					460				
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Met	Phe	Val	Leu	Ala	Pro	Asn	Ser	Met	Arg	Met	Ser	Leu	Val	Arg	His
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 <212> DNA
 <213> Potato

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 GTTAGTCGCC ATTTACTGCA CGAGGAGTTA CTCAAAAGGT GTGTGGAGGC AGGTGTTTTG 180
 TATCTAAACT CGAAAGTGGA TAGGATTGTT GAGGCCACAA ATGGCCACAG TCTTGTAGAG 240
 TGCGAGGGTG ATGTTGTGAT TCCCTGCAGG TTTGTGACTG TTGCATCGGG AGCAGCCTCG 300
 GGGAAATTCT TGCAGTATGA GTTGGGAGGT CCTAGAGTTT CTGTTCAAAC AGCTTATGGA 360
 GTGGAAGTTG AGGTCGATAA CAATCCATTT GACCCGAGCC TGATGGTTTT CATGGATTAT 420
 AGAGACTATG TCAGACACGA CGCTCAATCT TTAGAAGCTA AATATCCAAC ATTTCTCTAT 480
 GCCATGCCCA TGTCTCCAAC ACGAGTCTTT TTCGAGGAAA CTTGTTTGGC TTCAAAAGAT 540
 GCAATGCCAT TCGATCTGTT AAAGAAAAAA TTGATGTTAC GATTGAACAC CCTCGGTGTA 600
 AGAATTAAAG AAATTTATGA GGAGGAATGG TCTTACATAC CAGTTGGAGG ATCTTTGCCA 660
 AATACAGAAC AAAAAACACT TGCATTTGGT GCTGCTGCTA GCATGGTTCA TCCAGCCACA 720
 GGTTATTTCAG TCGTCAGATC ACTGTCTGAA GCTCCAAAAT GCGCCTTCGT GCTTGCAAAT 780
 ATATTACGAC AAAATCATAG CAAGAATATG CTTACTAGTT CAAGTACCCC GAGTATTTCA 840
 ACTCAAGCTT GGAACACTCT TTGGCCACAA GAACGAAAAC GACAAAGATC GTTTTTCCTA 900

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ACCTCATGTT ATTTGCCTTC TACATGTTTA TTATTGCACC AAATGACATG AGAAGAGGCT      1080
TAATCAGACA TCTTTTATCT GATCCTACTG GTGCAACATT GATAAGAACT TATCTTACAT      1140
TTTAGAGTAA ATTCCTCCTA CAATAGTTGT TGAAAGAGGC CTCATTACTT CAGATTCATA      1200
ACAGAAATCG CGGTCTCTCG AGGCCTTGTA TATAACATTT TCACTAGGTT AATATTGCTT      1260
GAATAAGTTG CACAGTTTCA GTTTTTGTAT CTGCTTCTTT TTTGTCCAAG ATCATGTATT      1320
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<210> 25
 <211> 377
 <212> PRT
 <213> Potato

<400> 25

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Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu
          35           40           45
Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn Ser Lys Val Asp
          50           55           60
Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val Glu Cys Glu Gly
          65           70           75           80
Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala Ser Gly Ala Ala
          85           90           95
Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Ser Val
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Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn Asn Pro Phe Asp
          115          120          125
Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Val Arg His Asp
          130          135          140
Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro
          145          150          155          160
Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys
          165          170          175
Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Leu Arg Leu
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Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu Glu Glu Trp Ser
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Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Thr Leu
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 Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser
 225 230 235 240
 Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala Phe Val Leu Ala
 245 250 255
 Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu Thr Ser Ser Ser
 260 265 270
 Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu
 275 280 285
 Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu
 290 295 300
 Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg
 305 310 315 320
 Val Pro Lys Met Met Trp Gly Phe Leu Gly Ser Ser Leu Ser Xaa Ala
 325 330 335
 Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn Asp
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<211> 533

<212> PRT

<213> Chimeric lettuce/potato

<400> 26

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 35 40 45
 Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val Val Asp Lys Gln
 50 55 60
 Gly Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser
 65 70 75 80
 Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser Met Glu Ser Gln
 85 90 95
 Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile Gly Asn Cys Ile
 100 105 110
 Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala

115					120					125					
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130						135					140				
Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Gln	Asp	Glu	Phe	Ile	Gly
145					150					155					160
Leu	Gly	Leu	Glu	Gly	Cys	Ile	Glu	His	Ser	Trp	Lys	Asp	Thr	Leu	Val
				165					170					175	
Tyr	Leu	Asp	Asp	Ala	Asp	Pro	Ile	Arg	Ile	Gly	Arg	Ala	Tyr	Gly	Arg
			180					185					190		
Val	His	Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu
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Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala
	210					215					220				
Pro	Asn	Gly	Tyr	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	Thr	Ile	Pro
225					230					235					240
Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu
				245					250					255	
Glu	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly
			260					265					270		
Val	Glu	Val	Glu	Val	Asp	Asn	Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val
		275					280					285			
Phe	Met	Asp	Tyr	Arg	Asp	Tyr	Val	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu
	290					295					300				
Ala	Lys	Tyr	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg
305					310					315					320
Val	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe
				325					330					335	
Asp	Leu	Leu	Lys	Lys	Lys	Leu	Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val
			340					345					350		
Arg	Ile	Lys	Glu	Ile	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly
		355					360					365			
Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala
	370					375					380				
Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu
385					390					395					400
Ser	Glu	Ala	Pro	Lys	Cys	Ala	Phe	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln
				405					410					415	
Asn	His	Ser	Lys	Asn	Met	Leu	Thr	Ser	Ser	Ser	Thr	Pro	Ser	Ile	Ser
			420					425					430		
Thr	Gln	Ala	Trp	Asn	Thr	Leu	Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg
		435					440					445			

Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu
 450 455 460

Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg Val Pro Lys Trp Met
 465 470 475 480

Trp Gln Gly Phe Leu Gly Ser Ser Leu Ser Xaa Ala Asp Leu Met Leu
 485 490 495

Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn Asp Met Arg Arg Gly
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Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly Ala Thr Leu Ile Arg
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Thr Tyr Leu Thr Phe
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 35 40 45

Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val
 50 55 60

Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val Ala Cys Asp
 65 70 75 80

Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala
 85 90 95

Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro Arg Val Cys
 100 105 110

Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Ser Pro Tyr
 115 120 125

Asp Pro Asp Gln Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Asn Glu
 130 135 140

Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro Thr Phe Leu Tyr Ala Met
 145 150 155 160

Pro Met Thr Lys Ser Arg Leu Phe Phe Glu Glu Thr Cys Leu Ala Ser
 165 170 175

Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu Met Leu Arg
 180 185 190

Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu Glu Glu Trp

195	200	205
Ser Tyr Ile Pro Val Gly Gly 210 215	Ser Leu Pro Asn Thr Glu Gln Lys Asn 220	
Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr 225 230 235 240		
Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala Ser Val Ile 245 250 255		
Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn Ser Asn Ile 260 265 270		
Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg Lys Arg Gln 275 280 285		
Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Phe Asp Thr 290 295 300		
Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu Pro Lys Trp 305 310 315 320		
Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly Asp Leu Val 325 330 335		
Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn Leu Arg Lys 340 345 350		
Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala Thr Met Ile 355 360 365		
Lys Thr Tyr Leu Lys Val 370		

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<211> 1002

<212> DNA

<213> Adonis palaestina

<400> 28

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GGAATGGATG CTGTTTCAGAA GCGGCTCATG TTCGACGACG AATGTATTTT GGTGGATGAG	180
AATGACAAGG TCGTCGGGCA TGATTCCAAA TACAACTGTC ATTTGATGGA AAAGATAGAG	240
GCAGAAAATT TGCTTCACAG AGCCTTCAGT GTTTTCTTGT TCAACTCAA ATATGAATTG	300
CTTCTTCAGC AACGATCCGC CACAAAGGTA ACATTCCCGC TCGTATGGAC AAACACATGT	360
TGCAGTCATC CTCTCTTTTCG TGATTCCGAG CTCATAGAAG AAAATTATCT CGGTGTACGA	420
AACGCTGCAC AAAGAAAGCT TTTAGACGAG CTAGGCATTC CAGCTGAAGA TGTCCCAGTT	480
GATGAATTTA CTCCTCTTGG TCGCATTCTT TACAAAGCTC CATCTGACGG CAAATGGGGA	540
GAGCACGAAT TGGACTATCT CCTATTTATT GTCCGAGATG TGAAATACGA TCCAAACCCA	600

GATGAAGTTG	CTGATGCTAA	GTATGTTAAT	CGCGAGGAGT	TGAGAGAGAT	ACTGAGAAAA	660
GCTGATGCTG	GTGAAGAGGG	ACTCAAGTTG	TCTCCTTGGT	TTAGATTGGT	TGTTGATAAC	720
TTTTTGTTC	AGTGGTGGA	TCATGTAGAG	CAGGGTACGA	TTAAGGAAGT	TGCTGACATG	780
AAACTATCC	ACAAGTTGAC	TTAAGAGGAC	TTCTCTCCTC	TGTTCTACTA	TTTGTTTTTT	840
GCTACAATAA	GTGGGTGGTG	ATAAGCAGTT	TTTCTGTTTT	CTTTAATTTA	TGGCTTTTGA	900
ATTTGCCTCG	ATGTTGAACT	TGTAACATAT	TTAGACAAAT	ATGAGACCTT	GTAAGTTGAA	960
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<211> 1271

<212> DNA

<213> Adonis palaestina

<400> 29

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TAAACCAGTA	ATTCTCGGTT	TTAATTTGTT	TCCTAAATTA	GGCCCCTTTC	CGGAATCCCG	180
AGAATTATGT	CGTCGATCAG	GATTAATCCT	TTATATAGTA	TCTTCTCCAC	CACCACTAAA	240
ACATTATCAG	CTTCGTGTTT	TTCTCCCGCT	GTTTCATCTT	AGCAGCGTTG	TACGTACTCT	300
TTCTATTTCT	TCTTCCATCA	CTAACAGTCC	TCGCCGAGGG	TTGAATCGGC	TGTTCGCCTC	360
AACGTCGACT	ATGGGTGAAG	TCGCTGATGC	TGGTATGGAT	GCCGTCCAGA	AGCGGCTTAT	420
GTTTCGACGAT	GAATGTATTT	TGGTGGATGA	GAATGACAAG	GTCGTCGGAC	ATGATTCCAA	480
ATACAACTGT	CATTTGATGG	AAAAGATAGA	GGCAGAAAAC	TTGCTTCACA	GAGCCTTCAG	540
TGTTTTCTTA	TTCAACTCAA	AATACGAGTT	GCTTCTTCAG	CAACGATCTG	CAACGAAGGT	600
AACATTCCCG	CTCGTATGGA	CAAACACCTG	TTGCAGCCAT	CCCCTCTTCC	GTGATTCCGA	660
ACTCATAGAA	GAAAATTTTC	TCGGGGTACG	AAACGCTGCA	CAAAGGAAGC	TTTTAGACGA	720
GCTAGGCATT	CCAGCTGAAG	ACGTACCAGT	TGATGAATTC	ACTCCTCTTG	GTCGCATTCT	780
TTACAAAGCT	CCATCTGACG	GAAAATGGGG	AGAGCACGAA	CTGGACTATC	TTCTGTTTAT	840
TGTCCGAGAT	GTGAAATACG	ATCCAAACCC	AGATGAAGTT	GCTGACGCTA	AGTACGTTAA	900
TCGCGAGGAG	TTGAAAGAGA	TACTGAGAAA	AGCTGATGCA	GGTGAAGAGG	GAATAAAGTT	960
GTCTCCTTGG	TTTAGATTGG	TTGTGGATAA	CTTTTGTTC	AAGTGGTGGG	ATCATGTAGA	1020
GGAGGGGAAG	ATTAAGGACG	TCGCCGACAT	GAAAACATATC	CACAAGTTGA	CTTAAGAGAA	1080
AGTCTCTTAA	GTTCTACTAT	TTGGTTTTTG	CTTCAATAAG	TGGATGGTGA	TGAGCAGTTT	1140
TTATGCTTCC	TTTAATTTTG	GCTTTTCAAT	TTGCTTTATG	TGTTGAACTT	GTAACATATT	1200
TAGTCAAATA	TGAGACCTTG	TGAGTTGAAT	TTGAGGTTAT	ATTTATAGTT	TTGGGAACAT	1260

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 <213> *Haematococcus pluvialis*
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 ACGCATATCC CGCGCGTGAA CTCCGCCCAG CAGCCCAGCT GTGCACACGC GCGACTCCAG 120
 TTTAAGCTCA GGAGCATGCA GCTGCTTGCC GAGGACCGCA CAGACCACAT GAGGGGTGCA 180
 AGCACCTGGG CAGGCGGGCA GTCGCAGGAT GAGCTGATGC TGAAGGACGA GTGCATCTTA 240
 GTGGATGCTG ACGACAACAT CACAGGCCAT GCCAGCAAGC TGGAGTGCCA CAAATTCCTA 300
 CCACATCAGC CTGCAGGCCT GCTGCACCGG GCCTTCTCTG TGTTCCTGTT TGACGACCAG 360
 GGGCGACTGC TGCTGCAACA GCGTGACGC TCAAAAATCA CCTTCCCAAG TGTGTGGACG 420
 AACACCTGCT GCAGCCACCC TCTACATGGG CAGACCCCAG ATGAGGTGGA CCAACTAAGC 480
 CAGGTGGCCG ACGGCACAGT ACCTGGCGCA AAAGCTGCTG CCATCCGCAA GTTGGAGCAC 540
 GAGCTGGGGA TACCAGCGCA CCAGCTGCCG GCAAGCGCGT TTCGCTTCCT CACGCGTTTG 600
 CACTACTGTG CCGCGGACGT GCAGCCGGCT GCGACACAAT CAGCGCTCTG GGGCGAGCAC 660
 GAGATGGACT ACATCTTATT CATCCGGGCC AACGTCACCT TGGCGCCCAA CCCTGACGAG 720
 GTGGACGAAG TCAGGTACGT GACGCAAGAG GAGCTGCGGC AGATGATGCA GCCGGACAAC 780
 GGGTTGCAAT GGTCGCCGTG GTTTCGCATC ATCGCCGCGC GCTTCCTTGA GCGTTGGTGG 840
 GCTGACCTGG ACGCGGCCCT AAACACTGAC AAACACGAGG ATGGGGGAAC GGTGCATCAC 900
 ATCAACGAAG CGTGAAGGCA GAAGCTGCAG GATGTGAAGA CACGTCATGG GGTGGAATTG 960
 CGTACTTGGC AGCTTCGTAT CTCCTTTTTC TGAGACTGAA CCTGCAGAGC TAGAGTCAAT 1020
 GGTGCATCAT ATTCATCGTC TCTCTTTTGT TTTAGACTAA TCTGTAGCTA GAGTCACTGA 1080
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 <211> 985
 <212> DNA
 <213> *Lactuca sativa*
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 TAGTGTTTTT CTCCACCCTC TTTCGTCTGC CGCTATGGGC GATTCCAGCA TGGATGCTGT 180
 CCAGCGACGT CTCATGTTCT ATGACGAATG CATTTTGGTG GATGAGAATG ACAAAGTGGT 240
 TGGCCATGAT ACTAAATACA ATTGTCATTT GATGGAGAAG ATTGAAAAGG GAAATATGCT 300

ACACAGAGCA TTCAGTGTGT TCTTGTTCAA CTCGAAATAT GAATTACTCC TTCAGCAACG 360
 TTCTGCAACC AAGGTGACTT TCCCTTTGGT ATGGACAAAC ACGTGTTGCA GCCATCCACT 420
 ATACAGGGAG AGTGAGCTTA TTGACGAAAA CGCCCTTGGG GTGAGGAATG CTGCACAGAG 480
 GAAGCTCCTG GATGAACTCG GCATCCCTGG AGCAGATGTT CCGGTTGATG AGTTCACTCC 540
 ATTGGGTCGC ATTCTATACA AGGCCGCATC GGATGGAAAG TGGGGAGAAC ATGAACTTGA 600
 TTACCTGCTG TTTATGGTAC GTGATGTTGG TTTGGATCCG AACCCAGATG AAGTGAAAGA 660
 TGTAATAATAT GTGAACCGGG AAGAGCTGAA GGAATTGGTA AGGAAGGCGG ATGCTGGTGA 720
 AGAGGGTGTG AAGCTGTCCC CGTGGTTCAA ATTGATTGTC GATAATTTCT TGTTCAGTG 780
 GTGGGATCGA CTCCATAAGG GAACCCTAAC CGAAGCTATT GATATGAAAA CAATCCACAA 840
 ACTCACATAA AAACACTACA CTAGTAGGAG AGAGGATTAT ATGAGATATT TGTTATATGT 900
 GAAATTGAAA TTCAGATGAA TGCTTGATT TATTTCTATT TGGACAAACT TCAACTTCTT 960
 TTTGCTACCT TATCAGAAAA AAAAA 985

<210> 32

<211> 988

<212> DNA

<213> *Lactuca sativa*

<400> 32

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 CTGTCCAGAG ACGTCTCATG TTTGATGATG AATGCATTTT GGTTGATGAA AATGACAATG 180
 TTCTTGGGCA TGATACCAAA TACAATTGTC ACTTGATGGA GAAGATTGAG AAAGATAATT 240
 TGCTTCATAG AGCATTCAGT GTATTTTAT TCAATTCAA ATACGAATTA CTCCTTCAGC 300
 AAAGGTCAGA AACCAAGGTG ACATTCCTT TGGTATGGAC AAACACCTGT TGCAGCCATC 360
 CACTATACAG AGAATCGGAG TTAATCCCG AAAATGCCCT TGGGGTCAGA AATGCTGCAC 420
 AGAGGAAGCT TCTAGATGAA CTCGGTATCC CTGCTGAAGA TGTTCCAGTT GATGAGTTCA 480
 CAACTTTAGG TCGCATGTTG TACAAGGCTC CATCTGATGG AAAATGGGGT GAACATGAAG 540
 TTGATTACCT ACTCTTCCTC GTGCGTGACG TTGCCGTGAA CCCAAACCCT GATGAGGTGG 600
 CGGACATTAG ATACGTGAAC CAAGAAGAGT TAAAGAGTT ACTAAGGAAG GCGGATGCGG 660
 GTGAGGAGGG TTTGAAATTG TCCCCATGGT TTAGGCTAGT GGTGGACAAC TTCTTGTTCA 720
 AATGGTGGGA TCATGTCCAA AAGGGGACAC TCAATGAAGC AATTGACATG AAAACCATTC 780
 ATAAGTTGAT ATGAAAAATG GTTAATATTT ATGGTGGTGG TTTGGAGCTA ATAATTTGTG 840
 TGTTCAAGTC TCGGTCCTTC TTTTTTAAAC GTTTTTTTTT TTTCTTTTAT TGGGAGTGTT 900
 TATTGTGTAC TTGTAACGTA GGCCCTTTGG TTACGCTTTA AGAGTTTAAT AAAGAACCAC 960

CGTTAATTTA AAAAAAAAAA AAAAAAAAA 988

<210> 33
 <211> 1874
 <212> DNA
 <213> Chlamydomonas reinhardtii

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 CTACCGAGCA GCATTGCTTT AGATCGCTTT GATGTCATAA ACTCCCACTT ATATGAGATC 180
 CAGTTTCATC GAGCCCAAGC CCAGAGCGCA ACCTGTCTTA AGCCGCGGCA GGGCGTCCAT 240
 GCGCCTCGCG CAAAGCCGTG CTCTCGTTGC GCGTGTGAGC TCCGCCCTGT GGCCGGGAGC 300
 AGGACTTTCA CAGGCTCAAA GCGTTGCGGT GCGAATGGCG AGTTCGTCAA CCTGGGAAGG 360
 CACGGGCCTG AGCCAGGATG ACTTCATGCA GCGGGACGAG TGCTTGGTGG TGGACGAGCA 420
 GGACCGGCTG CTAGGCACCG CCAACAAGTA CGACTGCCAC CGCTTCGAGG CGGCCAAGGG 480
 CCAGCCCTGC GGCCGCCTGC ACCGCGCCTT CTCCGTGTTC CTGTTCAGCC CCGACGGCCG 540
 ACTGCTGCTG CAGCAGCGCG CAGCCAGCAA GGTGACGTTT CCGGGTGTGT GGACCAACAC 600
 CTGCTGCTCG CACCCGCTGG CGGGCCAGGC GCCGGACGAG GTGGACCTGC CGGCGGCGGT 660
 AGCCTCGGGC CAGGTGCCGG GCATCAAGGC GGC GGCGGTG CGCAAGCTGC AGCACGAGCT 720
 GGGGATACCG CCGGAGCAGG TTCCCGCCTC CTCCTTCTCC TTCCTCACGC GTCTGCACTA 780
 CTGCGCCGCC GACACCGCCA CGCACGGCCC GCGGGCGGAG TGGGGCGAGC ACGAGGTGGA 840
 CTACGTGCTG TTCGTGCGGC CGCAGCAGCC CGTCAGCCTG CAGCCCAACC CAGACGAGGT 900
 GGACGCCACG CGCTACGTGA CGCTGCCGGA GCTTCAGTCC ATGATGGCGG ACCCCGGCCT 960
 CAGCTGGAGC CCCTGGTTCC GCATCCTGGC CACACAGCCC GCCTTCCTGC CCGCCTGGTG 1020
 GGGCGACCTG AAGCGGCGCT GGCGCCCGGG CGGCAGCCGA CTGTGCGACT GGGGCACCAT 1080
 CCACCGCGTC ATGTGAAGAA AAAGGGGAAG CAGGGGCGGG AGCGGGGGAT GAATGGGAAT 1140
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 CGGGCGTGAG CGTGTGTGTA CGTGAGCGAC AAAGCCGGGA GGCGGACCGC GCGATGGGTA 1260
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 GCGGCTGCAG GGGTATGTGG GCACCCGGGC ACGGAGGAGA AGGCACACGC AGGTGGCGCG 1380
 GAGGTGTGTC AGGGGCCATG GGCGGGCCTC ACTCCTGGTC GTGCCAGTG GTCTCGTGGG 1440
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 TCACTTGGTG AGGTGGGGCG AGGTGGCTGT GGGCGGCGGG CGCAGTGGCA GAAGGACACG 1560
 GTGTGTGAGC GGTGGAGCTC TGGCCGTGCC GGCCGTGAGG GGCGGATAGC GATATGACGT 1620

TGTGCTTGGC CGCTGTAATG CGGGAGAATG TGCAGGCCGC GAGAAGCGGG CCGTGGCAGG 1680
 AGGCCGCAGG CTGCAGCACC CGTTGGGGAG GTGCCACCTG CAGGCGCGGC GCCGGGCGGG 1740
 CCTGAGTAAT GGGCGCCTGA GTAGTGGCGG CCACAGGAGG CGCAGGAGGC AGCAGCAGGA 1800
 GGACGAGCTG GAGGGACCCG TTGGCAACCC AAGGTTGCGC GTGTAACATA GTGGCCATAC 1860
 AAAAAAAAAA AAAA 1874

<210> 34
 <211> 954
 <212> DNA
 <213> *Tagetes erecta*

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 ACAATGTGGT GGGACATGAT ACCAAATACA ATTGTCACCT GATGGAGAAG ATTGAAACAG 180
 GTAAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAATAC GAGTTACTTC 240
 TTCAGCAACG GTCTGCAACC AAGGTGACAT TTCCTTTAGT ATGGACCAAC ACCTGTTGCA 300
 GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAA CGCCCTTGGA GTAAGAAATG 360
 CTGCACAGAG GAAGCTGTTG GATGAACTCG GTATCCCTGC TGAAGATGTT CCCGTTGATC 420
 AGTTTACTCC TTTAGGTCGC ATGCTCTACA AGGCTCCATC TGATGGAAAG TGGGGAGAAC 480
 ATGAACTTGA CTACCTACTT TTCATAGTGA GAGACGTTGC TGTAACCCG AACCCAGATG 540
 AAGTGGCGGA TATCAAATAT GTGACCAGAA GAGTTAAAGG AGCTGCTAAG GAAAGCAGAT 600
 GCGGGGGAGG AGGGTTTGAA GCTGTCTCCA TGGTTCAGGT TAGTGGTTGA TAACTTCTTG 660
 TTCAAGTGGT GGGATCATGT GCAAAGGGT AACTCACTG AAGCAATTGA TATGAAAACC 720
 ATACACAAGC TGATATAGAA ACACACCCTC AACCGAAAAG TTCAAGCCTA ATAATTCGGG 780
 TTGGGTCGGG TCTACCATCA ATTGTTTTTT TCTTTTAAGA AGTTTTAATC TCTATTTGAG 840
 CATGTTGATT CTTGTCTTTT GTGTGTAAGA TTTTGGGTTT CGTTTCAGTT GTAATAATGA 900
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<210> 35
 <211> 1031
 <212> DNA
 <213> *Oryza sativa*

<400> 35
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 GAATGCATTT TGGTGGATGA ACAAGACAAT GTTGTGGCC ATGAATCAAA ATATAACTGC 180
 CATCTGATGG AAAAAATCGA ATCTGAAAAAT CTACTTCATA GGGCTTTCAG TGTATTCCTG 240

TTCAACTCAA AATATGAACT CCTACTCCAG CAACGATCTG CAACAAAGGT TACATTTTCCT 300
 CTAGTTTGGG CCAACACTTG CTGCAGCCAT CCTCTGTACC GTGAGTCTGA GCTTATACAG 360
 GAAAACTACC TTGGTGTTAG AAATGCTGCT CAGAGGAAGC TCTTGATGA GCTGGGCATC 420
 CCAGCTGAAG ATGTGCCAGT TGACCAATTC ACCCCTCTTG GTCGGATGCT TTACAAGGCC 480
 CCATCTGATG GAAAATGGGG TGAACACGAG CTTGACTACC TGCTGTTTCAT CGTCCGCGAC 540
 GTGAAGGTAG TCCCGAACCC GGACGAAGTG GCCGATGTGA AATACGTGAG CCGTGAGCAG 600
 CTGAAGGAGC TCATCCGCAA AGCGGACGCC GGAGAGGAAG GCCTGAAGCT GTCTCCCTGG 660
 TTCCGGCTGG TTGTTGACAA CTTCTCATG GGCTGGTGGG ATCACGTCGA GAAAGGCACC 720
 CTCAACGAGG CCGTGGACAT GGAGACCATC CACAAGCTGA AGTAAGGACT GCGATGTTGT 780
 GGCTGGAAAG AATGATCCTG AAGACTCTGT TCTTGTGCTG CTGCATATTA CTCTTACCAG 840
 GGAAGTTGCA GAAGTCAGAA GAAGCTTTTG TATGTTTCTG GGTTTGGAGC TTGGAAGTGT 900
 TGGGCTCTGC TGAAGTGAAG ATTCCTTAT AGAGTGTCTA TGTTAATTTA GCAAACCTCT 960
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<210> 36

<211> 232

<212> PRT

<213> Tagetes erecta

<400> 36

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 Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Thr Gly Lys
 35 40 45
 Met Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu
 50 55 60
 Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val
 65 70 75 80
 Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
 85 90 95
 Val Pro Glu Asn Ala Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu
 100 105 110
 Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp Gln Phe
 115 120 125
 Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp
 130 135 140

Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Ala
 145 150 155 160
 Val Asn Pro Asn Pro Asp Glu Val Ala Asp Ile Lys Tyr Val Ser His
 165 170 175
 Glu Glu Leu Lys Glu Leu Leu Arg Lys Ala Asp Ala Gly Glu Glu Gly
 180 185 190
 Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Phe
 195 200 205
 Lys Trp Trp Asp His Val Gln Lys Gly Thr Leu Thr Glu Ala Ile Asp
 210 215 220
 Met Lys Thr Ile His Lys Leu Ile
 225 230

<210> 37

<211> 280

<212> PRT

<213> Lactuca Sativa

<400> 37

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 20 25 30
 Pro Ser Leu Ala Ala Ala Ser Val Phe Leu His Pro Leu Ser Ser Ala
 35 40 45
 Ala Met Gly Asp Ser Ser Met Asp Ala Val Gln Arg Arg Leu Met Phe
 50 55 60
 Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val Gly His
 65 70 75 80
 Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Lys Gly Asn
 85 90 95
 Met Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu
 100 105 110
 Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val
 115 120 125
 Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
 130 135 140
 Ile Asp Glu Asn Ala Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu
 145 150 155 160
 Leu Asp Glu Leu Gly Ile Pro Gly Ala Asp Val Pro Val Asp Glu Phe
 165 170 175
 Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Ala Ser Asp Gly Lys Trp
 180 185 190
 Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Met Val Arg Asp Val Gly

195					200					205					
Leu	Asp	Pro	Asn	Pro	Asp	Glu	Val	Lys	Asp	Val	Lys	Tyr	Val	Asn	Arg
210						215					220				
Glu	Glu	Leu	Lys	Glu	Leu	Val	Arg	Lys	Ala	Asp	Ala	Gly	Glu	Glu	Gly
225					230					235					240
Val	Lys	Leu	Ser	Pro	Trp	Phe	Lys	Leu	Ile	Val	Asp	Asn	Phe	Leu	Phe
				245					250					255	
Gln	Trp	Trp	Asp	Arg	Leu	His	Lys	Gly	Thr	Leu	Thr	Glu	Ala	Ile	Asp
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Met	Lys	Thr	Ile	His	Lys	Leu	Thr								
	275						280								
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<213> Lactuca Sativa															
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			20					25					30		
Asp	Thr	Lys	Tyr	Asn	Cys	His	Leu	Met	Glu	Lys	Ile	Glu	Lys	Asp	Asn
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	50					55					60				
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65					70					75					80
Trp	Thr	Asn	Thr	Cys	Cys	Ser	His	Pro	Leu	Tyr	Arg	Glu	Ser	Glu	Leu
				85					90					95	
Ile	Pro	Glu	Asn	Ala	Leu	Gly	Val	Arg	Asn	Ala	Ala	Gln	Arg	Lys	Leu
			100					105					110		
Leu	Asp	Glu	Leu	Gly	Ile	Pro	Ala	Glu	Asp	Val	Pro	Val	Asp	Glu	Phe
		115					120					125			
Thr	Thr	Leu	Gly	Arg	Met	Leu	Tyr	Lys	Ala	Pro	Ser	Asp	Gly	Lys	Trp
	130					135					140				
Gly	Glu	His	Glu	Val	Asp	Tyr	Leu	Leu	Phe	Leu	Val	Arg	Asp	Val	Ala
145					150					155					160
Val	Asn	Pro	Asn	Pro	Asp	Glu	Val	Ala	Asp	Ile	Arg	Tyr	Val	Asn	Gln
				165					170					175	
Glu	Glu	Leu	Lys	Glu	Leu	Leu	Arg	Lys	Ala	Asp	Ala	Gly	Glu	Glu	Gly
			180					185					190		
Leu	Lys	Leu	Ser	Pro	Trp	Phe	Arg	Leu	Val	Val	Asp	Asn	Phe	Leu	Phe
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 <213> Adonis Palaestina
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 35 40 45
 Arg Arg Gly Leu Asn Arg Leu Phe Ala Ser Thr Ser Thr Met Gly Glu
 50 55 60
 Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu Met Phe Asp
 65 70 75 80
 Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val Gly Tyr Asp
 85 90 95
 Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala Glu Asn Leu
 100 105 110
 Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu
 115 120 125
 Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val Trp
 130 135 140
 Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser Glu Leu Ile
 145 150 155 160
 Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu Leu
 165 170 175
 Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp Glu Phe Thr
 180 185 190
 Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly
 195 200 205
 Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Lys Tyr
 210 215 220
 Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val Asn Arg Glu
 225 230 235 240
 Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu Glu Gly Ile
 245 250 255
 Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Phe Lys

260

265

270

Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val Ala Asp Met
 275 280 285

Lys Thr Ile His Lys Leu Thr
 290 295

<210> 40

<211> 234

<212> PRT

<213> Adonis Palaestina

<400> 40

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 20 25 30

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95

Glu Leu Ile Glu Glu Asn Tyr Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125

Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140

Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175

Asn Arg Glu Glu Leu Arg Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190

Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205

Leu Phe Lys Trp Trp Asp His Val Glu Gln Gly Thr Ile Lys Glu Val
 210 215 220

Ala Asp Met Lys Thr Ile His Lys Leu Thr
 225 230

<210> 41

<211> 238

<212> PRT

<213> Oryza Sativa

<400> 41

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Asp Asn Val Val Gly His Glu Ser Lys Tyr Asn Cys His Leu Met Glu
          35          40          45

Lys Ile Glu Ser Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu
          50          55          60

Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys
          65          70          75          80

Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu
          85          90          95

Tyr Arg Glu Ser Glu Leu Ile Gln Glu Asn Tyr Leu Gly Val Arg Asn
          100          105          110

Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp
          115          120          125

Val Pro Val Asp Gln Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala
          130          135          140

Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe
          145          150          155          160

Ile Val Arg Asp Val Lys Val Val Pro Asn Pro Asp Glu Val Ala Asp
          165          170          175

Val Lys Tyr Val Ser Arg Glu Gln Leu Lys Glu Leu Ile Arg Lys Ala
          180          185          190

Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val
          195          200          205

Val Asp Asn Phe Leu Met Gly Trp Trp Asp His Val Glu Lys Gly Thr
          210          215          220

Leu Asn Glu Ala Val Asp Met Glu Thr Ile His Lys Leu Lys
          225          230          235

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<210> 42

<211> 233

<212> PRT

<213> Arabidopsis thaliana

<400> 42

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Met Thr Asp Ser Asn Asp Ala Gly Met Asp Ala Val Gln Arg Arg Leu
 1          5          10          15

Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Asn Asn Arg Val Val
          20          25          30

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Gly His Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45
 Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60
 Tyr Glu Leu Leu Leu Gln Gln Arg Ser Lys Thr Lys Val Thr Phe Pro
 65 70 75 80
 Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser
 85 90 95
 Glu Leu Ile Glu Glu Asn Val Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110
 Lys Leu Phe Asp Glu Leu Gly Ile Val Ala Glu Asp Val Pro Val Asp
 115 120 125
 Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140
 Lys Trp Gly Glu His Glu Val Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160
 Val Lys Leu Gln Pro Asn Pro Asp Glu Val Ala Glu Ile Lys Tyr Val
 165 170 175
 Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp Ala Gly Asp
 180 185 190
 Glu Ala Val Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205
 Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Ile Thr Glu Ala
 210 215 220
 Ala Asp Met Lys Thr Ile His Lys Leu
 225 230

<210> 43

<211> 293

<212> PRT

<213> Haematococcus pluvialis

<400> 43

Met Leu Arg Ser Leu Leu Arg Gly Leu Thr His Ile Pro Arg Val Asn
 1 5 10 15
 Ser Ala Gln Gln Pro Ser Cys Ala His Ala Arg Leu Gln Phe Lys Leu
 20 25 30
 Arg Ser Met Gln Leu Leu Ser Glu Asp Arg Thr Asp His Met Arg Gly
 35 40 45
 Ala Ser Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys
 50 55 60
 Asp Glu Cys Ile Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala
 65 70 75 80
 Ser Lys Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu

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<210> 44
<211> 304
<212> PRT
<213> Haematococcus pluvialis
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<400> 44																
Met	Leu	Arg	Ser	Leu	Leu	Arg	Gly	Leu	Thr	His	Ile	Pro	Arg	Val	Asn	
1				5					10					15		
Ser	Ala	Gln	Gln	Pro	Ser	Cys	Ala	His	Ala	Arg	Leu	Gln	Phe	Lys	Leu	
			20					25					30			
Arg	Ser	Met	Gln	Met	Thr	Leu	Met	Gln	Pro	Ser	Ile	Ser	Ala	Asn	Leu	
		35					40					45				
Ser	Arg	Ala	Glu	Asp	Arg	Thr	Asp	His	Met	Arg	Gly	Ala	Ser	Thr	Trp	
	50					55					60					
Ala	Gly	Gly	Gln	Ser	Gln	Asp	Glu	Leu	Met	Leu	Lys	Asp	Glu	Cys	Ile	
65					70					75					80	

Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala Ser Lys Leu Glu
 85 90 95
 Cys His Lys Phe Leu Pro His Pro Ala Gly Leu Leu His Arg Ala Phe
 100 105 110
 Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln Arg
 115 120 125
 Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn Thr Cys Cys
 130 135 140
 Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp Gln Leu Ser
 145 150 155 160
 Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala Ala Ile Arg
 165 170 175
 Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu Pro Ala Ser
 180 185 190
 Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val Gln
 195 200 205
 Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp Tyr
 210 215 220
 Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp Glu
 225 230 235 240
 Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met Met
 245 250 255
 Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile Ala
 260 265 270
 Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala Ala Leu Asn
 275 280 285
 Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile Asn Glu Ala
 290 295 300

<210> 45

<211> 307

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 45

Met Arg Ser Ser Phe Ile Glu Pro Lys Pro Arg Ala Gln Pro Val Leu
 1 5 10 15
 Ser Arg Gly Arg Ala Ser Met Arg Leu Ala Gln Ser Arg Ala Leu Val
 20 25 30
 Ala Arg Val Ser Ser Ala Leu Trp Pro Gly Ala Gly Leu Ser Gln Ala
 35 40 45
 Gln Ser Val Ala Val Arg Met Ala Ser Ser Ser Thr Trp Glu Gly Thr
 50 55 60
 Gly Leu Ser Gln Asp Asp Phe Met Gln Arg Asp Glu Cys Leu Val Val

65	70	75	80
Asp Glu Gln Asp Arg Leu Leu Gly Thr Ala Asn Lys Tyr Asp Cys His	85	90	95
Arg Phe Glu Ala Ala Lys Gly Gln Pro Cys Gly Arg Leu His Arg Ala	100	105	110
Phe Ser Val Phe Leu Phe Ser Pro Asp Gly Arg Leu Leu Leu Gln Gln	115	120	125
Arg Ala Ala Ser Lys Val Thr Phe Pro Gly Val Trp Thr Asn Thr Cys	130	135	140
Cys Ser His Pro Leu Ala Gly Gln Ala Pro Asp Glu Val Asp Leu Pro	145	150	155
Ala Ala Val Ala Ser Gly Gln Val Pro Gly Ile Lys Ala Ala Ala Val	165	170	175
Arg Lys Leu Gln His Glu Leu Gly Ile Pro Pro Glu Gln Val Pro Ala	180	185	190
Ser Ser Phe Ser Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Thr	195	200	205
Ala Thr His Gly Pro Ala Ala Glu Trp Gly Glu His Glu Val Asp Tyr	210	215	220
Val Leu Phe Val Arg Pro Gln Gln Pro Val Ser Leu Gln Pro Asn Pro	225	230	235
Asp Glu Val Asp Ala Thr Arg Tyr Val Thr Leu Pro Glu Leu Gln Ser	245	250	255
Met Met Ala Asp Pro Gly Leu Ser Trp Ser Pro Trp Phe Arg Ile Leu	260	265	270
Ala Thr Gln Pro Ala Phe Leu Pro Ala Trp Trp Gly Asp Leu Lys Arg	275	280	285
Arg Trp Arg Pro Gly Gly Ser Arg Leu Ser Asp Trp Gly Thr Ile His	290	295	300
Arg Val Met	305		

<210> 46

<211> 1848

<212> DNA

<213> Adonis palaestina

<400> 46

GAGAGAAAAA GAGTGGTATA TTAATGTTAC TGTCGCATTC TTGCAACACA TATTCAGACT 60

CCATTTTCTT GTTTTCTCTT CAAAACAACA AACTAATGTG ACGGAGTATC TAGCTATGGA 120

ACTACTTGGT GTTCGCAACC TCATCTCTTC TTGCCCTGTC TGGACTTTTG GAACAAGAAA 180

CCTTAGTAGT TCAAACTAG CTTATAACAT ACATCGATAT GGTTCTTCTT GTAGAGTAGA 240


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TTTTCAAGTG AGGGCTGATG GTGGAAGCGG GAGTAGAACT TCTGTTGCTT ATAAAGAGGG      300
TTTTGTGGAC GAGGAGGATT TTATCAAAGC TGGTGGTTCT GAGCTTTTGT TTGTCCAAAT      360
GCAGCAAACA AAGTCTATGG AGAAACAGGC CAAGCTCGCC GATAAGTTGC CACCAATACC      420
TTTCGGAGAA TCTGTGATGG ACTTG GTTGT AATAGGTTGT GGACCTGCTG GTCTTTCACT      480
GGCTGCAGAA GCTGCTAAGC TAGGCTTGAA AGTTGGCCTT ATTGGTCCTG ATCTTCCTTT      540
TACAAATAAT TATGGTGTGT GGAAGACGA GTTCAAAGAT CTTGGACTTG AACGTTGTAT      600
CGAGCATGCT TGGAAGGACA CCATCGTATA TCTTGACAAT GATGCTCCTG TCCTTATTGG      660
TCGTGCATAT GGACGAGTTA GCCGGCATTG GCTGCATGAA GAGTTGCTGA AAAGGTGTGT      720
CGAGTCAGGT GTATCATATC TGAATTCTAA AGTGGAAAAG ATCACTGAAG CTGGTGATGG      780
CCATAGTCTT GTAGTTTGTG AAAACGACAT CTTTATCCCT TGCAGGCTTG CTACTGTTGC      840
ATCTGGAGCA GCTTCAGGGA AACTTTTGGG GTATGAAGTA GGTGGCCCTC GTGTTTGTGT      900
CCAAACTGCT TATGGTGTGG AGGTTGAGGT GGAGAACAAT CCATACGATC CCAACTTAAT      960
GGTATTTATG GACTACAGAG ACTATATGCA ACAGAAATTA CAGTGCTCGG AAGAAGAATA     1020
TCCAACATTT CTCTATGTCA TGCCCATGTC GCCAACAAGA CTTTTTTTTG AGGAAACCTG     1080
TTTGGCCTCA AAAGATGCCA TGCCTTTCGA TCTACTGAAG AGAAACTAA TGTCACGATT     1140
GAAGACTCTG GGTATCCAAG TTACAAAAAT TTATGAAGAG GAATGGTCTT ATATTCCTGT     1200
TGGGGGTTCT TTACCAAACA CAGAGCAAAA GAACCTAGCA TTTGGTGCTG CAGCAAGCAT     1260
GGTGCATCCA GCAACAGGCT ATTCGGTTGT ACGATCACTA TCAGAAGCTC CAAAATATGC     1320
TTCTGTAATT GCAAAGATTT TGAAGCAAGA TAACTCTGCA TATGTGGTTT CTGGACAAAG     1380
CAGTGCAGTA AACATTTCAA TGCAAGCATG GAGCAGTCTT TGGCCAAAGG AGCGAAAACG     1440
TCAAAGAGCA TTCTTTCTTT TCGGGTTAGA GCTTATTGTG CAGCTAGATA TTGAAGCAAC     1500
CAGAACGTTT TTTAGAACCT TCTCCGCTT GCCAACTTGG ATGTGGTGGG GTTTCCTTGG     1560
GTCTTCACTA TCATCTTTCT ATCTTGATTT GTTTTCCATG TACATGTTTG TTTTGGCCCC     1620
GAACAGCATG AGGATGTCAC TTGTGAGACA TTTGCTTTCA GATCCTTCTG GTGCAGTTAT     1680
GGTTAAAGCT TACCTCGAAA GGTAATCTGT TTTATGAAAC TATAGTGTCT CATTAAATAA     1740
ATGAGGATCC TTCGTATATG TATATGATCA TCTCTATGTA TATCCTATAT TCTAATCTCA     1800
TAAAGTAATC GAAAATTCAT TGATAGAAAA AAAAAAAAAA AAAAAAAAAA     1848

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<210> 47

<211> 529

<212> PRT

<213> Adonis palaestina

<400> 47

Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp

1	5	10	15
Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile	20	25	30
His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp	35	40	45
Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val	50	55	60
Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val	65	70	75
Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp	85	90	95
Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val	100	105	110
Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys	115	120	125
Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn	130	135	140
Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg	145	150	155
Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp	165	170	175
Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu	180	185	190
Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr	195	200	205
Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser	210	215	220
Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr	225	230	235
Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly	245	250	255
Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val	260	265	270
Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg	275	280	285
Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr	290	295	300
Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu	305	310	315
Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg	325	330	335

Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
 340 345 350
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 355 360 365
 Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
 370 375 380
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
 385 390 395 400
 Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
 405 410 415
 Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
 420 425 430
 Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
 435 440 445
 Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
 450 455 460
 Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
 465 470 475 480
 Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
 485 490 495
 Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
 500 505 510
 Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
 515 520 525

Arg

<210> 48
 <211> 378
 <212> PRT
 <213> Potato

<400> 48
 Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile Glu His Val Trp
 1 5 10 15
 Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro Ile Leu Ile Gly
 20 25 30
 Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu
 35 40 45
 Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn Ser Lys Val Asp
 50 55 60
 Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val Glu Cys Glu Gly
 65 70 75 80
 Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala Ser Gly Ala Ala
 85 90 95

Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Ser Val
 100 105 110
 Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn Asn Pro Phe Asp
 115 120 125
 Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Val Arg His Asp
 130 135 140
 Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro
 145 150 155 160
 Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys
 165 170 175
 Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Leu Arg Leu
 180 185 190
 Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu Glu Glu Trp Ser
 195 200 205
 Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Thr Leu
 210 215 220
 Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser
 225 230 235 240
 Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala Phe Val Leu Ala
 245 250 255
 Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu Thr Ser Ser Ser
 260 265 270
 Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu
 275 280 285
 Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu
 290 295 300
 Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg
 305 310 315 320
 Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Ser Leu Ser Xaa
 325 330 335
 Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn
 340 345 350
 Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly
 355 360 365
 Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 370 375

<210> 49

<211> 524

<212> PRT

<213> Arabidopsis thaliana

<400> 49

Met Glu Cys Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr
 1 5 10 15
 Phe Pro Ser Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr
 20 25 30
 Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
 35 40 45
 Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
 50 55 60
 Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
 65 70 75 80
 Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
 85 90 95
 Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
 100 105 110
 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
 115 120 125
 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
 130 135 140
 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
 145 150 155 160
 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
 165 170 175
 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
 180 185 190
 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
 195 200 205
 Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
 210 215 220
 Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
 225 230 235 240
 Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
 245 250 255
 Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
 260 265 270
 Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
 275 280 285
 Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
 290 295 300
 Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
 305 310 315 320
 Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys

325 330 335
 Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
 340 345 350
 Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
 355 360 365
 Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
 370 375 380
 His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
 385 390 395 400
 Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
 405 410 415
 Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
 420 425 430
 Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
 435 440 445
 Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
 450 455 460
 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
 465 470 475 480
 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
 485 490 495
 Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
 500 505 510
 Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
 515 520

<210> 50
 <211> 529
 <212> PRT
 <213> Adonis palaestina

<400> 50
 Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
 1 5 10 15
 Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
 20 25 30
 His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
 35 40 45
 Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
 50 55 60
 Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
 65 70 75 80
 Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp

85										90					95				
Lys	Leu	Pro	Pro	Ile	Pro	Phe	Gly	Glu	Ser	Val	Met	Asp	Leu	Val	Val				
			100					105					110						
Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ser	Leu	Ala	Ala	Glu	Ala	Ala	Lys				
		115					120					125							
Leu	Gly	Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn				
	130					135					140								
Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Glu	Arg				
145					150					155					160				
Cys	Ile	Glu	His	Ala	Trp	Lys	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asn	Asp				
				165					170					175					
Ala	Pro	Val	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu				
			180					185					190						
Leu	His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr				
		195					200					205							
Leu	Asp	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Gly	Asp	Gly	His	Ser				
	210					215					220								
Leu	Val	Val	Cys	Glu	Asn	Glu	Ile	Phe	Ile	Pro	Cys	Arg	Leu	Ala	Thr				
225					230					235					240				
Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly				
				245					250					255					
Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val				
			260					265					270						
Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Asn	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg				
		275					280					285							
Asp	Tyr	Met	Gln	Gln	Lys	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Tyr	Pro	Thr				
	290					295					300								
Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Arg	Leu	Phe	Phe	Glu	Glu				
305					310					315					320				
Thr	Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Arg				
				325					330					335					
Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	Leu	Gly	Ile	Gln	Val	Thr	Lys	Val				
			340					345					350						
Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn				
		355					360					365							
Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His				
	370					375					380								
Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys				
385					390					395					400				
Tyr	Ala	Ser	Val	Ile	Ala	Lys	Ile	Leu	Lys	Gln	Asp	Asn	Ser	Ala	Tyr				
				405					410					415					

Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
 420 425 430
 Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
 435 440 445
 Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
 450 455 460
 Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
 465 470 475 480
 Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
 485 490 495
 Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
 500 505 510
 Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
 515 520 525

Arg

<210> 51
 <211> 529
 <212> PRT
 <213> Adonis palaestina

<400> 51
 Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
 1 5 10 15
 Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
 20 25 30
 His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
 35 40 45
 Gly Gly Ser Gly Ser Arg Thr Ser Val Ala Tyr Lys Glu Gly Phe Val
 50 55 60
 Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
 65 70 75 80
 Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
 85 90 95
 Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
 100 105 110
 Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
 115 120 125
 Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
 130 135 140
 Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
 145 150 155 160

Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
 165 170 175
 Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
 180 185 190
 Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
 195 200 205
 Leu Asn Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
 210 215 220
 Leu Val Val Cys Glu Asn Asp Ile Phe Ile Pro Cys Arg Leu Ala Thr
 225 230 235 240
 Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
 245 250 255
 Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
 260 265 270
 Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
 275 280 285
 Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
 290 295 300
 Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
 305 310 315 320
 Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
 325 330 335
 Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Ile
 340 345 350
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 355 360 365
 Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
 370 375 380
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
 385 390 395 400
 Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
 405 410 415
 Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
 420 425 430
 Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
 435 440 445
 Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
 450 455 460
 Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
 465 470 475 480
 Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr

485 490 495
 Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
 500 505 510
 Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Lys Ala Tyr Leu Glu
 515 520 525

Arg

<210> 52
 <211> 533
 <212> PRT
 <213> Lettuce

<400> 52
 Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr Met Ala Val Phe
 1 5 10 15
 Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His Lys Phe Ser Leu
 20 25 30
 Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser Ser Ser Leu Arg
 35 40 45
 Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val Val Asp Lys Gln
 50 55 60
 Gly Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser
 65 70 75 80
 Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser Met Glu Ser Gln
 85 90 95
 Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile Gly Asn Cys Ile
 100 105 110
 Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala
 115 120 125
 Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu Ile Gly Pro Asp
 130 135 140
 Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp Glu Phe Ile Gly
 145 150 155 160
 Leu Gly Leu Glu Gly Cys Ile Glu His Ser Trp Lys Asp Thr Leu Val
 165 170 175
 Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg Ala Tyr Gly Arg
 180 185 190
 Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu
 195 200 205
 Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala
 210 215 220
 Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro

225		230		235		240
Cys Arg Leu Ala Thr	Val Ala Ser Gly	Ala Ala Ser Gly	Lys Phe Leu			
	245		250		255	
Glu Tyr Glu Leu Gly	Gly Pro Arg Val	Cys Val Gln Thr	Ala Tyr Gly			
	260		265		270	
Ile Glu Val Glu Val	Glu Asn Asn Pro	Tyr Asp Pro Asp	Leu Met Val			
	275		280		285	
Phe Met Asp Tyr Arg	Asp Phe Ser Lys	His Lys Pro Glu	Ser Leu Glu			
	290		295		300	
Ala Lys Tyr Pro Thr	Phe Leu Tyr Val	Met Ala Met Ser	Pro Thr Lys			
	305		310		315	
Ile Phe Phe Glu Glu	Thr Cys Leu Ala	Ser Arg Glu Ala	Met Pro Phe			
	325		330		335	
Asn Leu Leu Lys Ser	Lys Leu Met Ser	Arg Leu Lys Ala	Met Gly Ile			
	340		345		350	
Arg Ile Thr Arg Thr	Tyr Glu Glu Glu	Trp Ser Tyr Ile	Pro Val Gly			
	355		360		365	
Gly Ser Leu Pro Asn	Thr Glu Gln Lys	Asn Leu Ala Phe	Gly Ala Ala			
	370		375		380	
Ala Ser Met Val His	Pro Ala Thr Gly	Tyr Ser Val Val	Arg Ser Leu			
	385		390		395	
Ser Glu Ala Pro Asn	Tyr Ala Ala Val	Ile Ala Lys Ile	Leu Arg Gln			
	405		410		415	
Asp Gln Ser Lys Glu	Met Ile Ser Leu	Gly Lys Tyr Thr	Asn Ile Ser			
	420		425		430	
Lys Gln Ala Trp Glu	Thr Leu Trp Pro	Leu Glu Arg Lys	Arg Gln Arg			
	435		440		445	
Ala Phe Phe Leu Phe	Gly Leu Ser His	Ile Val Leu Met	Asp Leu Glu			
	450		455		460	
Gly Thr Arg Thr Phe	Phe Arg Thr Phe	Phe Arg Leu Pro	Lys Trp Met			
	465		470		475	
Trp Trp Gly Phe Leu	Gly Ser Ser Leu	Ser Ser Thr Asp	Leu Ile Ile			
	485		490		495	
Phe Ala Leu Tyr Met	Phe Val Ile Ala	Pro His Ser Leu	Arg Met Glu			
	500		505		510	
Leu Val Arg His Leu	Leu Ser Asp Pro	Thr Gly Ala Thr	Met Val Lys			
	515		520		525	
Ala Tyr Leu Thr Ile						
	530					

<210> 53

<211> 526
 <212> PRT
 <213> Tomato

<400> 53

Met	Glu	Cys	Val	Gly	Val	Gln	Asn	Val	Gly	Ala	Met	Ala	Val	Leu	Thr
1				5					10					15	
Arg	Pro	Arg	Leu	Asn	Arg	Trp	Ser	Gly	Gly	Glu	Leu	Cys	Gln	Glu	Lys
			20					25					30		
Ser	Ile	Phe	Leu	Ala	Tyr	Glu	Gln	Tyr	Glu	Ser	Lys	Cys	Asn	Ser	Ser
		35					40					45			
Ser	Gly	Ser	Asp	Ser	Cys	Val	Val	Asp	Lys	Glu	Asp	Phe	Ala	Asp	Glu
	50					55					60				
Glu	Asp	Tyr	Ile	Lys	Ala	Gly	Gly	Ser	Gln	Leu	Val	Phe	Val	Gln	Met
	65				70					75					80
Gln	Gln	Lys	Lys	Asp	Met	Asp	Gln	Gln	Ser	Lys	Leu	Ser	Asp	Glu	Leu
				85					90					95	
Arg	Gln	Ile	Ser	Ala	Gly	Gln	Thr	Val	Leu	Asp	Leu	Val	Val	Ile	Gly
			100					105					110		
Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly
		115					120					125			
Leu	Asn	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr
	130					135					140				
Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Gln	Ala	Cys	Ile
	145				150					155					160
Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Glu	Pro
				165					170					175	
Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Phe	Leu	His
			180					185					190		
Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ala	Gly	Val	Leu	Tyr	Leu	Asn
		195					200					205			
Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu	Val
	210					215					220				
Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val	Ala
	225				230					235					240
Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser	Pro
				245					250					255	
Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp	Asn
			260					265						270	
Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr
		275					280					285			
Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	Leu
	290					295					300				

Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
 305 310 315 320
 Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
 325 330 335
 Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu
 340 345 350
 Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
 355 360 365
 Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
 370 375 380
 Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala
 385 390 395 400
 Ser Val Leu Ala Asn Ile Leu Arg Gln His Tyr Ser Lys Asn Met Leu
 405 410 415
 Thr Ser Ser Ser Ile Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu
 420 425 430
 Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu
 435 440 445
 Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
 450 455 460
 Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
 465 470 475 480
 Ser Leu Ser Ser Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
 485 490 495
 Ile Ala Pro Asn Asp Met Arg Lys Gly Leu Ile Arg His Leu Leu Ser
 500 505 510
 Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 515 520 525

<210> 54

<211> 516

<212> PRT

<213> Tagetes erecta

<400> 54

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
 1 5 10 15
 Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
 20 25 30
 Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45
 Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80
 Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95
 Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110
 Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125
 Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140
 Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
 145 150 155 160
 Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175
 Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
 180 185 190
 Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
 195 200 205
 Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
 210 215 220
 Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240
 Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255
 Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270
 Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285
 Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300
 Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320
 Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335
 Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350
 Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
 355 360 365
 Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380
 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn

385 390 395 400
 Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415
 Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430
 Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445
 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460
 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480
 Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495
 Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
 500 505 510
 Tyr Leu Thr Ile
 515

<210> 55
 <211> 501
 <212> PRT
 <213> Arabidopsis thaliana

<400> 55
 Met Asp Thr Leu Leu Lys Thr Pro Asn Lys Leu Asp Phe Phe Ile Pro
 1 5 10 15
 Gln Phe His Gly Phe Glu Arg Leu Cys Ser Asn Asn Pro Tyr His Ser
 20 25 30
 Arg Val Arg Leu Gly Val Lys Lys Arg Ala Ile Lys Ile Val Ser Ser
 35 40 45
 Val Val Ser Gly Ser Ala Ala Leu Leu Asp Leu Val Pro Glu Thr Lys
 50 55 60
 Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser
 65 70 75 80
 Gln Val Val Asp Leu Ala Ile Val Gly Gly Gly Pro Ala Gly Leu Ala
 85 90 95
 Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp
 100 105 110
 Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp
 115 120 125
 Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser
 130 135 140
 Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg

145		150		155		160
Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln						
		165		170		175
Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn						
		180		185		190
Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val						
		195		200		205
Lys Ile Gln Ala Ser Val Val Leu Asp Ala Thr Gly Phe Ser Arg Cys						
		210		215		220
Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala Tyr						
		225		230		235
Gly Ile Val Ala Glu Val Asp Gly His Pro Phe Asp Val Asp Lys Met						
		245		250		255
Val Phe Met Asp Trp Arg Asp Lys His Leu Asp Ser Tyr Pro Glu Leu						
		260		265		270
Lys Glu Arg Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe						
		275		280		285
Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro						
		290		295		300
Gly Leu Arg Met Glu Asp Ile Gln Glu Arg Met Ala Ala Arg Leu Lys						
		305		310		315
His Leu Gly Ile Asn Val Lys Arg Ile Glu Glu Asp Glu Arg Cys Val						
		325		330		335
Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly						
		340		345		350
Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met Val						
		355		360		365
Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn Ala Ile Val Arg						
		370		375		380
Tyr Leu Gly Ser Pro Ser Ser Asn Ser Leu Arg Gly Asp Gln Leu Ser						
		385		390		395
Ala Glu Val Trp Arg Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg						
		405		410		415
Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Asp						
		420		425		430
Ala Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Gln Pro His Tyr						
		435		440		445
Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val						
		450		455		460
Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu						
		465		470		475
						480

Ile Met Thr Lys Gly Thr Val Pro Leu Ala Lys Met Ile Asn Asn Leu
 485 490 495

Val Gln Asp Arg Asp
 500

<210> 56

<211> 502

<212> PRT

<213> Adonis palaestina

<400> 56

Met Asp Thr Leu Leu Arg Thr His Asn Lys Leu Glu Leu Leu Pro Thr
 1 5 10 15

Leu His Gly Phe Ala Glu Lys Gln His Leu Val Ser Thr Ser Lys Leu
 20 25 30

Gln Asn Gln Val Phe Arg Ile Ala Ser Arg Asn Ile His Pro Cys Arg
 35 40 45

Asn Gly Thr Val Lys Ala Arg Gly Ser Ala Leu Leu Glu Leu Val Pro
 50 55 60

Glu Thr Lys Lys Glu Asn Leu Glu Phe Asp Leu Pro Ala Tyr Asp Pro
 65 70 75 80

Ser Arg Gly Ile Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala
 85 90 95

Gly Leu Ala Ile Ala Gln Gln Val Ser Glu Ala Gly Leu Leu Val Cys
 100 105 110

Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val
 115 120 125

Trp Val Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr
 130 135 140

Thr Trp Ser Gly Ala Val Val Tyr Thr Asp Asp Asn Ser Lys Lys Tyr
 145 150 155 160

Leu Asp Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys
 165 170 175

Met Leu Gln Lys Cys Val Thr Asn Gly Val Lys Phe His Gln Ala Lys
 180 185 190

Val Ile Lys Val Ile His Glu Glu Ser Lys Ser Leu Leu Ile Cys Asn
 195 200 205

Asp Gly Ile Thr Ile Asn Ala Thr Val Val Leu Asp Ala Thr Gly Phe
 210 215 220

Ser Arg Cys Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln
 225 230 235 240

Val Ala Tyr Gly Ile Met Ala Glu Val Glu Glu His Pro Phe Asp Leu
 245 250 255

Asp Lys Met Leu Phe Met Asp Trp Arg Asp Ser His Leu Asn Glu Lys
 260 265 270
 Leu Glu Leu Lys Asp Lys Asn Arg Lys Ile Pro Thr Phe Leu Tyr Ala
 275 280 285
 Met Pro Phe Ser Ser Thr Lys Ile Phe Leu Glu Glu Thr Ser Leu Val
 290 295 300
 Ala Arg Pro Gly Leu Arg Phe Glu Asp Ile Gln Glu Arg Met Val Ala
 305 310 315 320
 Arg Leu Lys His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu
 325 330 335
 Arg Cys Val Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg
 340 345 350
 Val Val Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly
 355 360 365
 Tyr Met Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Lys Ser
 370 375 380
 Ile Val Gln Tyr Leu Gly Ser Asp Arg Ser Leu Ser Gly Asn Glu Leu
 385 390 395 400
 Ser Ala Glu Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln
 405 410 415
 Arg Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu
 420 425 430
 Gln Gly Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro His
 435 440 445
 Tyr Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu
 450 455 460
 Phe Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Ala Ser Arg Ile
 465 470 475 480
 Glu Ile Met Ala Lys Gly Thr Val Pro Leu Val Asn Met Met Asn Asn
 485 490 495
 Leu Ile Gln Asp Thr Asp
 500

<210> 57
 <211> 498
 <212> PRT
 <213> Pepper

<400> 57
 Met Asp Thr Leu Leu Arg Thr Pro Asn Asn Leu Glu Phe Leu His Gly
 1 5 10 15
 Phe Gly Val Lys Val Ser Ala Phe Ser Ser Val Lys Ser Gln Lys Phe
 20 25 30

64

355 360 365
 Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile Gln Tyr
 370 375 380
 Leu Ser Ser Glu Arg Ser His Ser Gly Asp Glu Leu Ser Ala Ala Val
 385 390 395 400
 Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu Phe Phe
 405 410 415
 Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala Thr Arg
 420 425 430
 Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp His Gly
 435 440 445
 Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe Gly Leu
 450 455 460
 Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu Ile Met Thr
 465 470 475 480
 Lys Gly Thr Leu Pro Leu Val His Met Ile Asn Asn Leu Leu Gln Asp
 485 490 495
 Lys Glu

<210> 58
 <211> 500
 <212> PRT
 <213> Tomato

<400> 58
 Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro
 1 5 10 15
 His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
 20 25 30
 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45
 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60
 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80
 Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95
 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
 100 105 110
 Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125
 Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp

130		135		140
Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His				
145		150		155
Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met				
		165		170
Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile				
		180		185
Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly				
		195		200
Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg				
		210		215
Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala				
225		230		235
Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys				
		245		250
Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp				
		260		265
Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro				
		275		280
Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg				
		290		295
Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu				
305		310		315
Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys				
		325		330
Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val				
		340		345
Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met				
		355		360
Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile				
		370		375
Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr				
385		390		395
Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu				
		405		410
Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala				
		420		425
Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp				
		435		440
His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe				
		450		455
				460

Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
 465 470 475 480
 Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu
 485 490 495
 Gln Asp Lys Glu
 500

<210> 59
 <211> 500
 <212> PRT
 <213> Tobacco

<400> 59
 Met Asp Thr Leu Leu Lys Thr Pro Asn Lys Leu Glu Phe Leu His Pro
 1 5 10 15
 Val His Gly Phe Ser Val Lys Ala Ser Ser Phe Asn Ser Val Lys Pro
 20 25 30
 His Lys Phe Gly Ser Arg Lys Ile Cys Glu Asn Trp Gly Lys Gly Val
 35 40 45
 Cys Val Lys Ala Lys Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60
 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80
 Gly Leu Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95
 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Val Ser Ile
 100 105 110
 Asp Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125
 Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
 130 135 140
 Ser Gly Thr Val Val Tyr Ile Asp Asp Asn Thr Thr Lys Asp Leu Asp
 145 150 155 160
 Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
 165 170 175
 Gln Lys Cys Ile Leu Asn Gly Val Lys Phe His His Ala Lys Val Ile
 180 185 190
 Lys Val Ile His Glu Glu Ala Lys Ser Met Leu Ile Cys Asn Asp Gly
 195 200 205
 Val Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg
 210 215 220
 Cys Leu Val Gln Tyr Asp Lys Pro Tyr Lys Pro Gly Tyr Gln Val Ala
 225 230 235 240

Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Thr Ser Lys
 245 250 255
 Met Val Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Asn Met Glu
 260 265 270
 Leu Lys Glu Arg Asn Arg Lys Val Pro Thr Phe Leu Tyr Ala Met Pro
 275 280 285
 Phe Ser Ser Asn Lys Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg
 290 295 300
 Pro Gly Leu Arg Met Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu
 305 310 315 320
 Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys
 325 330 335
 Val Ile Pro Met Gly Gly Ser Leu Pro Val Ile Pro Gln Arg Val Val
 340 345 350
 Gly Thr Gly Gly Thr Ala Gly Leu Val His Pro Ser Thr Gly Tyr Met
 355 360 365
 Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
 370 375 380
 His Tyr Leu Gly Ser Glu Lys Asp Leu Leu Gly Asn Glu Leu Ser Ala
 385 390 395 400
 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415
 Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430
 Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445
 His Gly Phe Leu Ser Ser Arg Leu Tyr Leu Pro Glu Leu Ile Phe Phe
 450 455 460
 Gly Leu Ser Leu Phe Ser Arg Ala Ser Asn Thr Ser Arg Ile Glu Ile
 465 470 475 480
 Met Thr Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn Asn Leu Leu
 485 490 495
 Gln Asp Thr Glu
 500

<210> 60
 <211> 511
 <212> PRT
 <213> Tagetes erecta

<400> 60
 Met Asp Thr Phe Leu Arg Thr Tyr Asn Ser Phe Glu Phe Val His Pro
 1 5 10 15

Ser Asn Lys Phe Ala Gly Asn Leu Asn Asn Leu Asn Gln Leu Asn Gln
 20 25 30
 Ser Lys Ser Gln Phe Gln Asp Phe Arg Phe Gly Pro Lys Lys Ser Gln
 35 40 45
 Phe Lys Leu Gly Gln Lys Tyr Cys Val Lys Ala Ser Ser Ser Ala Leu
 50 55 60
 Leu Glu Leu Val Pro Glu Ile Lys Lys Glu Asn Leu Asp Phe Asp Leu
 65 70 75 80
 Pro Met Tyr Asp Pro Ser Arg Asn Val Val Val Asp Leu Val Val Val
 85 90 95
 Gly Gly Gly Pro Ser Gly Leu Ala Val Ala Gln Gln Val Ser Glu Ala
 100 105 110
 Gly Leu Thr Val Cys Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp Pro
 115 120 125
 Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met Asp Leu Leu
 130 135 140
 Asp Cys Leu Asp Thr Thr Trp Ser Ser Ala Val Val Tyr Ile Asp Glu
 145 150 155 160
 Lys Ser Thr Lys Ser Leu Asn Arg Pro Tyr Ala Arg Val Asn Arg Lys
 165 170 175
 Gln Leu Lys Thr Lys Met Leu Gln Lys Cys Ile Ala Asn Gly Val Lys
 180 185 190
 Phe His Gln Ala Lys Val Ile Lys Val Ile His Glu Glu Leu Lys Ser
 195 200 205
 Leu Leu Ile Cys Asn Asp Gly Val Thr Ile Gln Ala Thr Leu Val Leu
 210 215 220
 Asp Ala Thr Gly Phe Ser Arg Ser Leu Val Gln Tyr Asp Lys Pro Tyr
 225 230 235 240
 Asn Pro Gly Tyr Gln Val Ala Tyr Gly Ile Leu Ala Glu Val Glu Glu
 245 250 255
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 Thr Phe Leu Tyr Ala Met Pro Phe Ser Ser Thr Arg Ile Phe Leu Glu
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 325 330 335
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 Cys Arg Asn Gly Tyr Ile Gly Val Ser Ser Asn Gln Leu Leu Asp Leu
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 65 70 75 80
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 85 90 95
 Pro Leu Ala Arg Ser Cys Ser Thr Ser Leu Gly Gly Gly Leu Ser Val
 100 105 110
 Val Ser Ile Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly

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Leu	Ser	Ala	Asp	Val	Trp	Lys	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg
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Gln	Arg	Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp
			420					425					430		
Leu	Glu	Gly	Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe	Phe	Asp	Leu	Glu	Pro
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Arg Tyr Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu
450 455 460

Val Pro Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Cys Lys
465 470 475 480

Leu Glu Ile Met Ala Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn
485 490 495

Asn Leu Val Gln Asp Arg Asp
500

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/12121

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 435/189, 193, 233, 252.3, 320.1, 325; 536/23.2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/189, 193, 233, 252.3, 320.1, 325; 536/23.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97/36998 A1 (UNIVERSITY OF MARYLAND COLLEGE PARK) 09 October 1997, see entire document, especially SEQ ID No:1.	1-8



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

03 AUGUST 1999

Date of mailing of the international search report

15 SEP 1999

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/12121

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 1/21, 5/10, 9/10, 15/53, 15/54, 15/61, 15/63; C12P 23/00; C12Q 1/68

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

Dialog and APS

search terms: IPP, epsilon cyclase, lycopene cyclase, isopentenyl pyrophosphate isomerase and isopentenyl diphosphate isomerase